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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : A61K 39/106, C07K 16/12, A61K 39/40 — A1

(11) International Publication Number: WO 96/34624

(43) International Publication Date: 7 November 1996 (07.11.96)

(21) International Application Number: PCT/EP96/01834

(22) International Filing Date: 2 May 1996 (02.05.96)

(30) Priority Data:

432,697	2 May 1995 (02.05.95)	US
447,177	19 May 1995 (19.05.95)	US

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(81) Designated States: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, ARIPO patent (KE, LS, MW, SD, SZ, UG), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

With international search report.

Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(54) Title: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID POLYPEPTIDES

(57) Abstract

There is provided an immunogenic composition capabale of inducing protective antibodies against *Helicobacter* infection characterized in that it comprises: i) at least one sub-unit of a urease structural polypeptide from *Helicobacter pylori*, or a fragment thereof, said fragment being recognized by antibodies reacting with *Helicobacter felis* urease, and/or at least one sub-unit of a urease structural polypeptide from *Helicobacter felis*, or a fragment thereof, said fragment being recognized by antibodies reacting with *Helicobacter pylori* urease; ii) and/or, a heat shock protein (Hsp), or chaperonin, from *Helicobacter*, or a fragment of said protein. The preparation, by recombinant means, of such immunogenic composition is also provided.

.NSDOCID: <WO___9634624A1_I_>

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IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID POLYPEPTIDES

Technical Field

The present invention relates to immunogenic compositions for inducing protective antibodies against *Helicobacter spp.* infection. It also relates to proteinaceous material derived from *Helicobacter*, and to nucleic acid sequences encoding them. Antibodies to these proteinaceous materials are also included in the invention.

Background Art

H. pylori is a microorganism, which infects human gastric mucosa and is associated with active chronic gastritis. It has been shown to be an aetiological agent in gastroduodenal ulceration (Peterson, 1991), and two recent studies have reported that persons infected with *H. pylori* had a higher risk of developing gastric cancer (Nomura et al., 1991; Parsonnet et al., 1991).

In vivo studies of the bacterium, and consequently, work on the development of appropriate preventive or therapeutic agents, has been severely hindered by the fact that *Helicobacter pylori* 18only associates with gastric-type epithelium from very few animal hosts, none of which are suitable for use as laboratory models.

A mouse model of gastric colonization has been developed using a helical bacterium isolated from cat gastric mucus (Lee et al., 1988, 1990) and identified as a member of the genus *Helicobacter.* It has been named *H. felis* (Paster et al., 1990).

To date, only limited information concerning *H. felis* and the extent of its similarities and differences with *H. pylori* is available. The reliability of the mouse

model for the development of treatments for *H. pylori* infection is, therefore, uncertain. Recently, it was shown that *H. pylori* urease is a protective antigen in the *H. felis/mouse* model (Davin et al., 1993; Corthesy-Theulaz et al., 1993).

It is, therefore, an aim of the present invention to provide therapeutic and preventive compositions for use in *Helicobacter* infection, which furthermore can be tested in laboratory animals.

It is known that *H. pylori* expresses urease activity and that urease plays an important role in bacterial colonization and mediation of certain pathogenic processes (Ferrero and Lee, 1991; Hazel et al., 1991).

The genes coding for the urease structural polypeptides of *H. pylori* (*UreA*, *UreB*) have been cloned and sequenced (Labigne et al., 1991; and French Patent Application FR 8813135), as have the genes coding the "accessory" polypeptides necessary for urease activity in *H. pylori* (International patent application WO 93/07273).

Attempts have been made to use nucleic acid sequences from the *H. pylori* urease gene cluster as probes to identify urease sequences in *H. felis*. However, none of these attempts have been successful. Furthermore, the establishment and maintenance of *H. felis* cultures *in vitro* is extremely difficult, and the large quantities of nucleases present in the bacteria complicates the extraction of DNA.

Disclosure of the Invention

The present inventors have, however, succeeded in cloning and sequencing the genes of the urease structural polypeptides of *H. felis*, and of the accessory polypeptides. This has enabled, in the context of the invention, the comparison of the amino acid sequence data for the *H. felis Ure* gene products with that for *Helicobacter pylori*, and a high degree of conservation between the urease sub-units has been found. An immunological relationship between the

two ureases exists, and protective antibodies to *Helicobacter* infection can be induced using the urease sub-units or fragments thereof as immunogens.

Indeed, to elucidate the efficiency of individual urease subunits to act as mucosal immunogens, the genes encoding the respective urease sub-units (*UreA* and *UreB*) of *Helicobacter pylori* and *Helicobacter felis* have been cloned in an expression vector (pMAL) and expressed in *Escherichia coli* cells as translational fusion proteins. The recombinant UreA and UreB proteins have been purified by affinity and anion exchange chromatography techniques, and have predicted molecular weights of approximately 68 and 103 kDa, respectively. Western blotting studies indicated that the urease components of the fusion proteins are strongly immunogenic and are specifically recognized by polyclonal rabbit anti-*Helicobacter* sera. Orogastric immunization of mice with 50 mm of recombinant *H. felis* UreB, administered in combination with a mucosal adjuvant (cholera toxin), protected 60% ($n = 7$; $p < 0.005$) of mice from gastric colonization by *H. felis* bacteria at over 4 months. This compared with a value of 25% ($n = 8$; $p > 0.05$) for the heterologous *H. pylori* UreB antigen. For the first time, a recombinant subunit antigen has been shown to induce an immunoprotective response against gastric *Helicobacter* infection.

The inventors have also identified, in the context of the invention, new heat shock proteins or chaperonins in *Helicobacter*, which have an enhancing effect on urease activity. Use of the chaperonins in an immunogenic composition may induce therefore an enhancement of protection.

Indeed, the genes encoding each of the HspA and HspB polypeptides of *Helicobacter pylori* have been cloned, expressed independently as fused proteins to the Maltose-Binding-Protein (MBP), and purified on a large scale. These proteins have been used as recombinant antigens to immunize rabbits, and in Western immunoblotting assays as well as ELISA, to determine their immunogenicity in patients infected with HP (HP+). The MBP-HspA and MBP-

HspB fusion proteins have been shown to retain their antigenic properties. Comparison of the humoral immune response against HspA and/or HspB in (HP-) patient sera demonstrated that not only HspB but also HspA was recognized by (HP+) patient sera (29/38 and 15/38 respectively). None of the 14 uninfected patients had antibodies reacting with the Hsps.

Brief Description Of The Figures

This invention will be described in greater detail by reference to the following drawings:

Fig. 1. Transposon mutagenesis and sequencing of pILL205. Linear restriction maps of recombinant cosmid pILL199 and recombinant plasmid pILL205 (and the respective scale markers) are presented. Numbers in parentheses indicate the sizes of *H. felis* DNA fragments inserted into one of the cloning vectors (pILL575 described in J. Bact. 1991, 173:1920-1931 or pILL570, described in Res. Microb. 1992, 143:1526, respectively). The "plus" and "minus" signs within circles correspond to the insertion sites of the MiniTn3-Km transposon in pILL205; "plus" signs indicate that the transposon did not inactivate urease expression, whereas negative signs indicate that urease expression was abolished. The letters refer to mutant clones, which were further characterized for quantitative urease activity and for the synthesis of urease gene products. The location of the structural urease genes (*UreA* and *UreB*) on pILL205 are represented by boxes, the lengths of which are proportional to the sizes of the respective open-reading frames. The arrows refer to the orientation of transcription. The scale at the bottom of the Figure indicates the sizes (in kilobases) of the *Hind*III and *Pst*I restriction fragments. Restriction sites are represented as follows:. B, *Bam*HI; Pv, *Pvu*II; Bg, *Bgl*II; E, *Eco*RI; H, *Hind*III; C, *Cla*I; Ps, *Pst*I. Letters within parentheses indicate that the sites originated from the cloning vector.

Fig. 2. Western blot analysis of whole-cell extracts of *E. coli* HB101 cells harboring recombinant plasmids were reacted with rabbit polyclonal antiserum (diluted 1:1, 1000) raised against *H. felis* bacteria.

A) Extracts were of *E. coli* cells harboring: plasmid vector pILL570 (lane 1); recombinant plasmid pILL205, described in Molec. Microb. 1993, 9:323-333 (lane 2); and pILL205 derivative plasmids disrupted in loci "a", "b", "c", "d", and "e" (lanes 3-7).

B) Extracts were of *E. coli* cells harboring: recombinant plasmid pILL753 containing the *H. pylori ure* A and *ure* B genes (Labigne et al., 1991) (lane 1); and pILL205 derivative plasmids disrupted in loci "f", "g", "h", and "i" (lanes 2-5). The small arrow heads indicate polypeptides of approximately 30 and 66 kilodaltons, which represent putative *UreA* and *UreB* gene products of *H. felis*. The large arrow heads in panel B indicate the corresponding gene products of *H. pylori*, which cross-reacted with the anti-*H. felis* serum. The numbers indicate the molecular weights (in thousands) of the protein standards.

Fig. 3. Nucleotide sequence of the *H. felis* structural urease genes. Numbers above the sequence indicate the nucleotide positions as well as the amino acid position in each of the two UreA and UreB polypeptides. Predicted amino acid sequences for UreA (bp 43 to 753) and UreB (766 to 2616) are shown below the sequence. The putative ribosome-binding site (Shine-Dalgarno sequence, SD) is underlined.

Fig. 4. Comparison of sequences for the structural urease genes of *H. felis* to:

a) the sequence of the two subunits of *H. pylori* urease (Labigne et al., 1991);

b) the sequence of the three subunits of *Proteus mirabilis* urease (Jones and Mobley, 1989);

c) the sequence of the single subunit of jack bean urease. Margin gaps (shown by dashes) have been introduced to ensure the best alignment. *, identical to those of the *H. felis* sequence; =, amino acids shared by ureases; , amino acids unique to the *Helicobacter* ases. The percent te to the number of amino acids that are identical t ase of the *H. felis* u nits. *H.f.*, *Helicobacter felis*; *H.p.*, *Helicobacter pylori*; *P.m.*, *Proteus mirabilis*, ck bean.

Fig. 5. Restriction map o recombinant plasmids pILL689, pILL685, and pILL691. The construction of these plasmids is described in detail in Table 5. Km within triangles depicts the site of insertion of the kanamycin cassette, which led to the construction of plasmids pILL687, pILL688, and pILL696 (Table 5). Boxes underneath the maps indicate the position of the three genetic elements deduced from the nucleotide sequence, namely IS5, *hsp* A and *hsp* B.

Fig. 6. Nucleotide sequence of the *Helicobacter pylori* heat shock protein gene cluster. The first number above the sequence indicates the nucleotide positions, whereas the second one numbers the amino acid residue position for each of the HspA and HspB protein. The putative ribosome-binding sequences (Shine-Dalgarno [SD] sites) are underlined.

Fig. 7. Comparison of the deduced amino-acid sequence of *Helicobacter pylori* HspA (A) or HspB (B) with that of other *Gro*EL-like (A) or GroES-like (B) proteins. Asterisks mark amino acids identical with those in the *Helicobacter pylori* HspA or HspB sequences.

Fig. 8. Expression of the *Helicobacter pylori* HspA heat shock proteins in *E. coli* minicells. The protein bands with apparent molecular masses of 58 and 13 kDA, corresponding to the *Helicobacter pylori* HspA and HspB heat shock proteins are clearly visible in the lanes corresponding to plasmids pILL689 and

pILL692 and absent in the vector controls (pILL570 and pACYC177, respectively).

Fig. 9. Nucleotide sequence of the *Helicobacter felis Ure* I gene and deduced amino acid sequence.

Fig. 10. Comparison of the amino acid sequence of the *Ure* I proteins deduced from the nucleotide sequence of the *Ure* I gene of *Helicobacter felis* and that of *Helicobacter pylori*.

Fig. 11. Genetic code. Chain-terminating, or "nonsense", codons. Also used to specify the initiator formyl-Met-$tRNA^{Met}_{F}$. The Val triplet GUG is therefore "ambiguous" in that it codes both valine and methionine.

Fig. 12. Signification of the one-letter and three-letter amino-acid abbreviations.

Fig. 13. Purification of *H. pylori* UreA-MBP recombinant protein using the pMAL expression vector system. Extracts from the various stages of protein purification were migrated on a 10% resolving SDS-polyacrylamide gel. Following electrophoresis, the gel was stained with Coomassie blue. The extracts were: 1) non-induced cells; 2) IPTG-induced cells; French press lysate of induced cell extract; 5) eluate from amylose resin column; 6) eluate from anion exchange column (first passage); 7) eluate from anion exchange column (second passage); and 8) SDS-PAGE standard marker proteins.

Fig. 14. Recognition of UreA recombinant fusion proteins by polyclonal rabbit anti-*Helicobacter* sera. Protein extracts of maltose-binding protein (MBP, lane 1), *H. felis* UreA-MBP (lane 2), and *H. pylori* UreA-MBP (lane 3) were Western blotted using rabbit polyclonal antisera (diluted 1:5000) raised against whole cell extracts of *H. pylori* and *H. felis*. The purified fusion proteins are indicated by an arrow. Putative degradation products of the proteins are shown by an asterisk.

Fig. 15. Recognition of UreB recombinant fusion proteins by rabbit antisera raised against purified homologous and heterologous UreB proteins. Nitrocellulose membranes were blotted with the following extracts: 1) standard protein markers; 2) *H. felis* UreA-MBP; 3) MBP; 4) *H. pylori* UreA-MBP. The membranes were reacted with polyclonal rabbit antisera (diluted 1:5000) raised against MBP-fused *H. pylori* and *H. felis* UreB sub-units, respectively. The molecular weights of standard proteins are presented on the left-hand side of the blots.

Fig. 16. Western blot analysis of *H. pylori* and *H. felis* whole cell extracts with antisera raised against purified UreB MBP-fused recombinant proteins. SDS-PAGE whole extracts of *H. Felis* (lane 1) and *H. pylori* (lane 2) cells were reacted with polyclonal rabbit antisera raised against purified *H. pylori* UreB and *H. felis* UreB MBP-fused proteins (sera diluted 1:5000). The difference in gel mobility of the respective non-recombinant UreB sub-units of *H. felis* and *H. pylori* can be seen. The numbers on the left refer to the molecular weights of standard marker proteins.

Fig. 17. SDS-PAGE analysis of material eluted from the amylose column (lanes 2 and 3) or from the Ni-NTA column following elution: with buffer E (pH 4.5), lanes 4 and 5; or buffer C (pH 6.3), lanes 6 and 7. Material eluted from a lysate of MC1061 (PILL933) (lanes 2, 3, 5, and 7) and material eluted from a lysate of MC1061 (PMAL-c2) (lanes 4 and 6). Lane 3 contains the same material as in lane 2 except that it was resuspended in buffer E, thus demonstrating that buffer E is responsible for dimer formation of the MBP-HspA subunit, as seen in lanes 3 and 5.

Fig. 18. Serum IgG responses to MBP (bottom), MBP-HspA (top) and MBP-HspB (middle) of 28 *H. pylori* infected patients (squares, left) and 12 uninfected patients (circles, right). The optical density of each serum in the ELISA assay described in Experimental Procedures was read at 492 nm, after a

30 mn incubation. The sizes of the symbols are proportional to the number of sera giving the same optical density value.

Fig. 19. Measurement by ELISA of serum antibodies (IgG_1 and IgG_{2a} isotypes) in mice immunized with recombinant *H. pylori* antigens. A_{492} values for individual serum samples (diluted 1:100) are presented. Horizontal lines represent the mean A_{492} values for each set of data.

Fig. 20. Immunoblot analyses of total cell extracts of *H. felis* (lane 1) and *H. pylori* (lane 2) using rabbit antisera raised against recombinant *H. pylori* HspA and HspB antigens (dilution 1:5000). Arrows refer to cross-reactive proteins: (I) monomeric and (ii) dimeric forms of HspA antibody-reactive proteins are indicated. Protein standards are indicated on the right-hand side of each of the blots (numbers are in kDa). Immunoreactants on the anti-HspA blotted membrane were revealed directly with a peroxidase-labelled secondary antibody, whilst antigens on the anti-HspB were detected using a biotinylated secondary antibody/streptavidin-peroxidase procedure. The latter was found to give higher background staining and when used to detect immunoreactants on membranes blotted with the anti-HspA antibody, produced very weak signals.

Best Mode for Carrying Out the Invention

An immunogenic composition capable of inducing antibodies against *Helicobacter* infection can be characterized in that it comprises:

i) at least one sub-unit of a urease structural polypeptide from *Helicobacter pylori*, or a fragment thereof, defined by two restriction sites or comprised between 6 to 100 amino acids or delineated by two specific oligonucleotides targeting any sequence of 300 bp, said fragment being recognized by antibodies reacting with *Helicobacter felis* urease, and/or at least one sub-unit of a urease structural polypeptide from *Helicobacter felis*, or a fragment thereof, said fragment being recognized by antibodies reacting with *Helicobacter pylori* urease;

ii) and/or a Heat Shock protein (Hsp), or chaperonin, from *Helicobacter*, or a fragment of said protein.

Preferably, the immunogenic composition is capable of inducing protective antibodies.

According to a preferred embodiment, the immunogenic composition of the invention contains, as the major active ingredient, at least one sub-unit of a urease structural polypeptide from *Helicobacter pylori* and/or *Helicobacter felis*. The expression "urease structural polypeptide" signifies, in the context of the present invention, the enzyme of *Helicobacter pylori* or *Helicobacter felis*, probably a major surface antigen composed of two repeating monomeric sub-units, a major sub-unit (product of the *UreB* gene) and a minor sub-unit product of the *UreA* gene, and which, when complemented by the presence of the products of the accessory genes of the urease gene cluster, are responsible for urease activity i.e., the hydrolysis of urea to liberate NH_4^+ in the two *Helicobacter* species. It is to be understood that in the absence of the accessory gene products, the urease structural polypeptides do not exhibit enzymatic activity, but are recognized by antibodies reacting with *H. felis* or *H. pylori* urease.

The term "immunogenic composition" signifies, in the context of the invention, a composition comprising a major active ingredient as defined above, together with any necessary ingredients to ensure or to optimize an immunogenic response, for example adjuvants, such as mucosal adjuvant, etc.

The *Helicobacter pylori* urease structural polypeptide has been described and sequenced by Labigne et al., 1991. The polypeptide described in this paper is particularly appropriate for use in the composition of the present invention. However, variants showing functional homology with this published sequence may be used, which comprise amino acid substitutions, deletions or insertions provided that the immunological characteristics of the polypeptide insofar as its cross-reactivity with anti-*Helicobacter felis* urease antibodies is concerned, are

maintained. Generally speaking, the polypeptide variant will show a homology of at least 75% and preferably about 90% with the included sequence.

A fragment of the *Helicobacter pylori* urease structural polypeptide may also be used in the immunogenic composition of the invention, or at least one sub-unit of a urease structural polypeptide from *Helicobacter pylori*, or a fragment thereof, defined by two restriction sites or comprised between 6 to 100 amino acids or delineated by two specific oligonucleotides targeting any sequence of 300 bp, provided that the fragments are recognized by antibodies reacting with *helicobacter felis* urease. Such a fragment will generally be comprised of at least 6 amino acids, for example, from 6 to 100 amino acids, preferably about 20-25. Advantageously, the fragment carries epitopes unique to *Helicobacter*.

Nucleic acid and amino-acid sequences may be interpreted in the context of the present invention by reference to Figs. 11 and 12, showing the genetic code and amino acid abbreviations respectively.

The *Helicobacter felis* urease structural polypeptide suitable for use in the present invention is preferably that encoded by part of the plasmid pILL205 (deposited at the CNCM on 25th August 1993, under number: CNCM I-1355), and whose amino acid sequence is shown in Fig. 3 (subunits A and B). Again, a variant of this polypeptide comprising amino acid substitutions, deletions or insertions with respect to the Fig. 3 sequence may be used provided that the immunological cross-relationship with *Helicobacter pylori* urease is maintained. Such a variant normally exhibits at least 90% homology or identity with the Fig. 3 sequence. An example of such variants are the urease A and B sub-units from *Helicobacter heilmannii* (Solnick et al., 1994), shown to have 80% and 92% identity with the *H. felis* urease A and B sub-units, respectively.

Fragments of this urease or variants may be used in the immunogenic composition provided that the fragments are recognized by antibodies reacting with *Helicobacter pylori* urease. Again, the length of such a fragment is usually

at least 6 amino acids, for example, from 6 to 100, preferably about 20 to 25. Preferably, the fragment carries epitopes unique to *Helicobacter*.

If variants or fragments of the native urease sequences are employed in the immunogenic composition of the invention, their cross-reactivity with antibodies reacting with urease from the other *Helicobacter* species can be tested by contacting the fragment or the variant with antibodies, preferably polyclonal raised to either the native or the recombinant urease or, alternatively, to whole *Helicobacter*. Preferably, the variants and fragments give rise to antibodies which are also capable of reacting with *H. heilmannii* urease. Cross protection to infection by *H. heilmannii* is therefore also obtained by the immunogenic composition of the invention.

The use of fragments of the urease structural genes is particularly preferred since the immunological properties of the whole polypeptide may be conserved whilst minimizing risk of toxicity.

The active component of the immunogenic composition of the invention may be comprised of one sub-unit only of the urease structural polypeptide, that is either sub-unit A or sub-unit B products of the *UreA* and *UreB* genes, respectively. Compositions comprising only the urease sub-unit UreB, of either *H. pylori* or *H. felis*, or variants and fragments as defined above, are particularly advantageous. Most preferred are homologous systems wherein the urease sub-unit, particularly sub-unit B, is derived from the organism against which protection is sought, e.g., *H. felis* sub-unit B against *H. felis* infection. However, the composition may contain both A and B sub-units, which are normally present as distinct polypeptides. However, it is possible, when the polypeptide is produced by recombinant means, to use a fusion protein comprising the entire sequences of the A and B gene products by the suppression of the stop-codon separating the two adjacent coding sequences.

The urease component of the immunogenic composition, whether sub-unit A or sub-unit B, may be used in the form of translational fusion proteins, for example with the Maltose-Binding-Protein (MBP). Other suitable fusions are exemplified in International Patent Application WO 90/11360. Another example of a suitable fusion protein is the "QIAexpress" system commercialized by QIAGEN, USA, which allows the 6xHis tag sequence to be placed at the 5' or 3' end of the protein coding sequence. The use of the active ingredients in the form of fusion proteins is, however, entirely optional.

According to a further preferred embodiment, the immunogenic composition of the invention may comprise in addition to or instead of the urease structural polypeptide defined above, a Heat Shock Protein also known as a "chaperonin" from *Helicobacter*. These chaperonins have been elucidated by the inventors in the context of the present invention. Preferably, the chaperonin is from *Helicobacter pylori*. Such an Hsp may be the urease-associated HspA or HspB or a mixture of the two, having the amino acid sequence illustrated in Fig. 6. These polypeptides are encoded by the plasmid pILL689 (deposited at CNCM on 25th August 1993, under number: CNCM I-1356). Particularly preferred is the *H. pylori* HspA protein, either alone or in combination with HspB.

It is also possible to use, as Hsp component, according to the invention, a polypeptide variant in which amino acids of the Fig. 6 sequence have been replaced, inserted or deleted, the said variant normally exhibiting at least 75%, and preferably at least 85% homology with the native Hsp. The variants preferably exhibit at least 75%, for example at least 85% identity with the native Hsp.

The variants may further exhibit functional homology with the native polypeptide. In the case of the Hsp components, "functional homology" means the capacity to enhance urease activity in a microorganism capable of expressing active urease, and/or the capacity to block infection by *Helicobacter*, particularly

H. felis and *H. pylori*. The property of enhancing urease activity may be tested using the quantitative urease activity assay described below in the examples. Fragments of either or both of the HspA and HspB polypeptides, preferably having at least 6 amino acids, may be used in the composition. The fragments or variants of the Hsp component used in the immunogenic composition of the invention are preferably capable of generating antibodies, which block the infection against *H. pylori* or *H. felix*. The presence of the chaperonins in the composition enhances the protection against *Helicobacter pylori* and *felis*.

The Hsp component of the immunogenic composition, whether HspA or HspB, can be used in the form of a translational fusion protein, for example with the Maltose-Binding-Protein (MBP). As for the urease component, other suitable fusion partners are described in International Patent Application WO 90/11360. The "QIAexpress" system of QIAGEN, USA, may also be used. Again, the use of the proteins in the form of fusion proteins is entirely optional.

According to the invention, therefore, the immunogenic composition may comprise either a urease structural polypeptide as defined above, or a *Helicobacter* Hsp, particularly HspA or a combination of these immunogens.

According to a preferred embodiment, the immunogenic composition comprises, as urease component or a fragment thereof, both the A and/or B sub-units or fragments of urease of *Helicobacter felis* (i.e., without *H. pylori* urease) the urease component can be associated or note to the Hsp A and/or Hsp B of *Helicobacter pylori*. Alternatively, the A and B sub-units of the *Helicobacter felis* urease may be used together with those of *H. pylori*, but without chaperonin component.

The immunological cross-reactivity between the ureases of the two different *Helicobacter* species enables the use of one urease only in the composition, preferably that of *Helicobacter felis*. The protective antibodies induced by the common epitopes will, however, be active against both

Helicobacter pylori and *Helicobacter felis*. It is also possible that the composition induce protective antibodies to other species of *Helicobacter* if the urease polypeptide or fragment carries epitopes occurring also on those other species.

In a preferred embodiment, the composition of the invention comprises a mixture of antigens of Helicobacter wherein said mixture consists essentially of UreB and HspA of H. pylori or polypeptides having at least 75 % and preferably 80 to 90 % similarity with said UreB or HspA, or fragments thereof capable of eliciting antibodies recognized by H. pylori or an immune cellular response against H.pylori infection.

In another specific embodiment of the invention, the composition comprises a mixture consisting essentially of ureB and HspA of H. felis or polypeptides having at least 75 % and preferably 80 to 90 % similarity with said UreB or HspA, or fragments thereof capable of inducing antibodies recognized by H. pylori and/or by H. felis or an immune cellular response against an H. pylori and/or H. felis infection.

The preparation of such antibodies is described for illustration in the examples.

The invention further relates to fragments having the above properties, which fragments comprise between 9 and 200 aminoacid residues. These fragments can be used for inducing antibodies. Such fragments can be prepared by usual synthesis for example as proposed by « Applied Biosystem »

As a preferred fragment for the preparation of the invention, the C-terminal sequence of HspA of H. pylori replying to the following amino-acid sequence is used:

G S C C H T G N H D H K H A K E H E A C C H D H K K H.

The composition of the invention preferably contains an amount of antigens or fragments thereof sufficient to elicit an immune response in a host to whom it is administered.

The response can be a cellular and/or a humoral immune response.

Advantageously the antigen or fragments thereof are recombinant antigens either in isolated form or included in fusion proteins. Some examples of antigens or genes encoding proteinaceous material suitable for the formation of fusion proteins are cited in the present description and should be regarded as appropriate for producing fusion proteins with UreB or HspA antigens or fragments thereof.

In a particular embodiment, the composition described hereabove is substantially free of UreA antigen and in another embodiment, is substantially of other H. pylori of H. felis antigens.

Further components can be added to the composition, including adjuvants and for instance a mucosal adjuvant, for example, cholera or E. coli holotoxins.

The composition described hereabove can be formulated as pharmaceutical composition; in such a case physiologically acceptable excipients may be added.

The composition of the invention is advantageously used as an immunogenic composition or a vaccine, together with physiologically acceptable excipients and carriers and, optionally, with adjuvants, haptens, carriers, stabilizers, etc. Suitable adjuvants include muramyl dipeptide (MDP), complete and incomplete Freund's adjuvants (CFA and IFA) and alum. The vaccine compositions are normally formulated for oral administration.

The vaccines are preferably for use in man, but may also be administered in non-human animals, for example for veterinary purposes, or for use in animals such as mice, cats and dogs.

They are in particular suitable for protecting against Helicobacter, especially H. pylori.

The immunogenic compositions administered by suitable routes into animals raises an immune response and especially raises the synthesis *in vivo* of specific antibodies, which can be used for therapeutic or curative purposes, for example in passive immunity.

Especially a composition comprising a mixture of UreB and HspA of H. pylori and/or H. felis or related polypeptides or fragments thereof is interesting for inducing or enhancing a protective response against mucosal infection by Helicobacter pylori in a host to whom it is administered.

The invention also relates to the proteinaceous materials used in the immunogenic composition and to proteinaceous material encoded by the urease gene clusters other than the A and B urease structural sub-units. "Proteinaceous material" means any molecule comprised of chains of amino acids, e.g., peptides, polypeptides or proteins, fusion or mixed proteins (i.e. an, association of 2 or more proteinaceous materials, all or some of which may have immunogenic or immunomodulation properties), either purified or in a mixture with other proteinaceous or non-proteinaceous material. "Polypeptide" signifies a chain of amino acids whatever its length and englobes the term "peptide". The term "fragment" means any amino acid sequence shorter by at least one amino acid than the parent sequence and comprising a length of amino acids, e.g., at least 6 residues, consecutive in the parent sequence.

The peptide sequences of the invention, may for example, be obtained by chemical synthesis, using a technique such as the Merrifield technique and synthesizer of the type commercialized by Applied Biosystems.

In particular, the invention relates to proteinaceous material characterized in that it comprises at least one of the *Helicobacter felis* polypeptides encoded by the urease gene cluster of the plasmid pILL205 (CNCM I-1355), including the

structural and accessory urease polypeptides, or a polypeptide having at least 90% homology with said polypeptides, or a fragment thereof. Of particular interest are the gene products of the *ure A* and *ure B* genes, as illustrated in Fig. 3, or a variant thereof having at least 90% homology or a fragment having at least 6 amino acids. The fragments and the variants are recognized by antibodies reacting with *Helicobacter pylori* urease.

Among the polypeptides encoded by the accessory genes of the urease gene cluster is the gene product of *Ure I*, as illustrated in Fig. 9, which also forms part of the invention. Also included is a variant of the *Ure I* product having at least 75% homology, preferably at least 85%, or a fragment of the gene product or of the variant having at least 6 amino acids. The variant preferably has the capacity to modulate the expression of urease activity. The urease activity can be detected by using the following test: 10^9 bacteria containing the *Ure I* gene product variant are suspended in 1 ml of urea-indole medium and incubated at 37° C. The hydrolysis of the urea leads to the release of ammonium, which increases pH and induces a color change from orange to fuscia-red.

It is also possible that a fragment of the *Ure I* gene product, if it has a length of, for example, at least 70 or 100 amino acids, may also exhibit this functional homology with the entire polypeptide.

The fragments of *Ure I* polypeptide or of the variant preferably are capable of inducing the formation of antibodies which interfere with the activiation process of the urease apoenyzme.

The invention also relates to the proteinaceous material comprising at least one of the heat shock proteins or chaperonins of *Helicobacter pylori* or a fragment thereof. Particularly preferred are the HspA and HspB polypeptides as illustrated in Fig. 6 or a polypeptide having at least 75%, and preferably at least 80 or 90%, homology or identity with the said polypeptide. A particularly

preferred fragment of the *Helicobacter pylori* HspA polypeptide is the C-terminal sequence:

G S C C H T G N H D H K H A K E H E A C C H D H K K H

or a sub-fragment of this sequence having at least 6 consecutive amino acids. This C-terminal sequence is thought to act as a metal binding domain allowing binding of, for example, nickel or divalent cations.

E. coli strains containing various subsets of the *H. pylori* urease subunits:

- *E. coli* MC1061 (pILL918) [CNCM registration number I-1336] expressing a UreA peptide (AA N°19 to AA N°238) fused to MalE

- *E. coli* MC1061 (pILL923) [CNCM registration number I-1338] expressing a UreA peptide (AA N°58 to AA N°238) fused to MalE

- *E. coli* MC1061 (pILL924) [CNCM registration number I-1339] expressing a UreA peptide (AA N°184 to AA N°238) fused to MalE

- *E. coli* MC1061 (pILL928) [CNCM registration number I-1341] expressing a UreA peptide (AA N°205 to AA N°569) fused to MalE

- *E. coli* MC1061 (pILL931) [CNCM registration number I-1342] expressing a UreA peptide (AA N°400 to AA N°569) fused to MalE

HspA and HspB of *H. felis* are detected as shown in Fig. 20. Antibodies raised against recognized MBP HspA or MBP HspB of *H. pylori* recognized HspA where HspB of *H. felis*.

The proteinaceous material of the invention may also comprise or consist of a fusion or mixed protein including at least one of the sub-units of the urease structural polypeptide of *H. pylori* and/or of *H. felis*, or fragments or variants thereof as defined above. Particularly preferred fusion proteins are the Mal-E fusion proteins and QIAexpress system fusion proteins (QIAGEN, USA) as detailed above. The fusion or mixed protein may include, either instead of or in

addition to the urease sub-unit, a Heat Shock Protein, or fragment or variant thereof, as defined above.

The invention also relates to monoclonal or polyclonal antibodies to the protein materials described above. More particularly, the invention relates to antibodies or fragments thereof to any one of the *Helicobacter felis* polypeptides encoded by the urease gene cluster of the plasmid pILL205 (CNCM I-1355), including the structural and accessory urease polypeptides, that is, structural genes *UreA* and *UreB* and the accessory genes known as *Ure* E, *Ure* F, *Ure* G, *Ure* H and *Ure* I. The antibodies may also be directed to a polypeptide having at least 90% homology with any of the above urease polypeptides or to a fragment thereof preferably having at least 6 amino acids. The antibodies of the invention may specifically recognize *Helicobacter felis* polypeptides expressed by the urease gene cluster. In this case, the epitopes recognized by the antibodies are unique to *Helicobacter felis*. Alternatively, the antibodies may include or consist of antibodies directed to epitopes common to *Helicobacter felis* urease polypeptides and to *Helicobacter pylori* urease polypeptides. If the antibodies recognize the accessory gene products, it is particularly advantageous that they cross-react with the *Helicobacter pylori* accessory gene product. In this way, the antibodies may be used in therapeutic treatment of *Helicobacter pylori* infection in man by blocking the urease maturation process.

Particularly preferred antibodies of the invention recognize the *Helicobacter felis UreA* and/or *UreB* gene products, that is the A and B urease sub-units. Advantageously, these antibodies also cross-react with the *Helicobacter pylori* A and B urease sub-units, but do not cross-react with other ureolytic bacteria. Such antibodies may be prepared against epitopes unique to *Helicobacter* (see Fig. 4), or alternatively, against the whole polypeptides followed by screening out of any antibodies reacting with other ureolytic bacteria.

The invention also concerns monoclonal or polyclonal antibodies to the Hsps or fragments thereof, particularly to the HspA and/or HspB protein illustrated in Figure 6. Polypeptides having at least 75%, and preferably at least 80%, or 90%, homology with the Hsps may also be used to induce antibody formation. These antibodies may be specific for the *Helicobacter pylori* or *H. felis* chaperonins or, alternatively, they may cross-react with GroEL-like proteins or GroES-like proteins from bacteria other than *Helicobacter*, depending upon the epitopes recognized. Fig. 7 shows the homologous regions of HspA and HspB with GroES-like proteins and GroEL-like proteins, respectively, from various bacteria. Particularly preferred antibodies are those specific for either the HspA or HspB chaperonins or those specifically recognizing the HspA C-terminal sequence having the metal binding function. Again, use of specific fragments for the induction of the antibodies ensures production of *Helicobacter*-specific antibodies.

The invention further relates to antibodies obtained against a composition comprising a mixture of UreB and HspA antigens of H. pylori, or a mixture of polypeptides having at least 75 %, preferably 80 or 90 % similarity with said UreB or HspA antigens, or fragments thereof.

These antibodies can be directed against one of the above antigens, or can be a mixture of antibodies against these different antigens of the composition.

Furthermore these antibodies are specific to H. pylori or to H. felis or to the contrary cross react with both strains.

The antibodies of the invention may be prepared using classical techniques. For example, monoclonal antibodies may be produced by the hybridoma technique, or by known techniques for the preparation of human antibodies, or by the technique described by Marks et al. (Journal of Molecular Biology, 1991, 222, p. 581-597).

The invention also includes fragments of any of the above antibodies produced by enzyme digestion. Of particular interest are the Fab and $F(ab')_2$ fragments. Also of interest are the Facb fragments.

The invention also relates to purified antibodies or serum obtained by immunization of an animal, e.g., a mammal, with the immunogenic composition, the proteinaceous material or fragment, or the fusion or mixed protein(s) of the invention, followed by purification of the antibodies or serum. Such protein can be the product of one of the genes of urease cluster either *H. pylori* or *H. felis* associated or not with the product of *Hsp*A or *Hsp*B of *H. pylori* or *H. felis* genes. Also concerned is a reagent for the *in vitro* detection of *H. pylori* infection containing at least these antibodies or serum, optionally with reagents for labelling the antibodies, e.g., anti-antibodies etc.

The invention further relates to nucleic acid sequences coding for any of the above proteinaceous materials including peptides. In particular, the invention relates to a nucleic acid sequence characterized in that it comprises:

i) a sequence coding for the *Helicobacter felis* and/or *H. pylori* urease and/or accessory polypeptides as defined above, and/or a sequence coding for the Hsp of *H. pylori* or *H. felis* as defined above; or

ii) a sequence complementary to sequence (i); or

iii) a sequence capable of hybridizing to sequence (i) or (ii) under stringent conditions; or

iv) a fragment of any of sequences (i), (ii) or (iii) comprising at least 10 nucleotides.

Preferred nucleic acid sequences are those comprising all or part of the sequence of plasmid pILL205 (CNCM I-1355), for example the sequence of Fig. 3, in particular that coding for the gene product of *UreA* and for *UreB* or the sequence of Fig. 9 (Ure I), or a sequence capable of hybridizing with these sequences under stringent conditions, or a sequence complementary to these

sequences, or a fragment comprising at least 10 consecutive nucleotides of these sequences.

Other preferred sequences are those comprising all or part of the sequence of plasmid pILL689 (CNCM I-1356), for example the sequence of Fig. 6, in particular that coding for *Hsp*A and/or *Hsp*B, or a sequence complementary to this sequence, or a sequence capable of hybridizing to this sequence under stringent conditions, or a fragment thereof.

High stringency hybridization conditions in the context of the invention are the following:

- 5 x SSC;
- 50% formamide at 37°C;

or:

- 6 x SSC;
- Denhard medium at 68°C.

The sequences of the invention also include those hybridizing to any of sequences (i), (ii) and (iii) defined above under non-stringent conditions, that is:

- 5 x SSC;
- 0.1% SDS;
- 30 or 40% formamide at 42°C, preferably 30%.

The term "complementary sequences" in the context of the invention signifies "complementary" and "reverse" or "inverse" sequences.

The nucleic acid sequences may be DNA or RNA.

The sequences of the invention may be used as nucleotide probes in association with appropriate labelling means. Such means include radioactive isotopes, enzymes, chemical or chemico-luminescent markers, fluorochromes, haptens, or antibodies. The markers may optionally be fixed to a solid support, for example a membrane or particles.

As a preferred marker, radioactive phosphorous (^{32}P) is incorporated at the 5'-end of the probe sequence. The probes of the invention comprise any fragment of the described nucleic acid sequences and may have a length for example of at least 45 nucleotides, for example 60, 80 or 100 nucleotides or more. Preferred probes are those derived from the *UreA, UreB, Ure* I, *HspA* and *HspB* genes.

The probes of the invention may be used in the *in vitro* detection of *Helicobacter* infection in a biological sample, optionally after a gene amplification reaction. Most advantageously, the probes are used to detect *Helicobacter felis* or *Helicobacter pylori*, or both, depending on whether the sequence chosen as the probe is specific to one or the other, or whether it can hybridize to both. Generally, the hybridization conditions are stringent in carrying out such a detection.

The invention also relates to a kit for the *in vitro* detection of *Helicobacter* infection, characterized in that it comprises:

- a nucleotide probe according to the invention, as defined above;

- an appropriate medium for carrying out a hybridization reaction between the nucleic acid of *Helicobacter* and the probe; and

- reagents for the detection of any hybrids formed.

The nucleotide sequences of the invention may also serve as primers in a nucleic acid amplification reaction. The primers normally comprise at least 10 consecutive nucleotides of the sequences described above and preferably at least 18. Typical lengths are from 25 to 30 and may be as high as 100 or more consecutive nucleotides. Such primers are used in pairs and are chosen to hybridize with the 5'- and 3'-ends of the fragment to be amplified. Such an amplification reaction may be performed using for example the PCR technique (European patent applications EP200363, 201184 and 229701). The Q-^b-

replicase technique (Biotechnology, vol. 6, Oct. 1988) may also be used in the amplification reaction.

The invention also relates to expression vectors characterized in that they contain any of the nucleic acid sequences of the invention. Particularly preferred expression vectors are plasmids pILL689 and pILL205 (CNCM I-1356 and CNCM I-1355, respectively). The expression vectors will normally contain suitable promoters, terminators and marker genes, and any other regulatory signals necessary for efficient expression.

The invention further relates to prokaryotic or eukaryotic host cells stably transformed by the nucleic acid sequences of the invention. As examples of hosts, mention may be made of higher eukaryotes such as CHO cells and cell-lines; yeast; prokaryotes including bacteria such as *E. coli*, e.g, *E. coli* HB 101, *Shigellae* or *Salmonella*, Mycobacterium tuberculosis, viruses including baculovirus and vaccinia. Usually the host cells will be transformed by vectors. However, it is also possible within the context of the invention to insert the nucleic acid sequences by homologous recombination, using conventional techniques. For example, WO 90.11354 (Brulet et al.) describes the technology to carry out an homologous recombination in eukaryotic cells.

By culturing the stably transformed hosts of the invention, the *Helicobacter* urease polypeptide material and, where applicable, the Hsp material can be produced by recombinant means. The recombinant proteinaceous materials are then collected and purified. Pharmaceutical compositions are prepared by combining the recombinant materials with suitable excipients, adjuvants, and optionally, any other additives, such as stabilizers.

The invention also relates to plasmids pILL920 (deposited at CNCM on 20.07.1993, under accession number I-1337) and pILL927 (CNCM I-1340, deposited on 20.07.1993) constructed as described in the examples below.

The invention covers also the DNA (or RNA derived from such DNA) purified from the expression vectors and used as immunogen capable of inducing an immune response in a host (cellular or antibody response).

Examples

I. Cloning, Expression And Sequencing Of *H. Felis* Urease Gene:

A. Experimental Procedures For Part I:

1. Bacterial strains and culture conditions:

H. felis (ATCC 49179) was grown on blood agar base no. 2 (Oxoid) supplemented with 5% (v/v) lysed horse blood (BioMerieux) and an antibiotic supplement consisting of 10 ng ml^{-1} vancomycin (Lederle Laboratories), 2.5 µg ml^{-1} polymyxin B (Pfizer), 5 µg ml^{-1} trimethoprim (Sigma Chemical Co.) and 2.5 µg ml^{-1} amphotericin B (E.R Squibb and Sons, Inc.). Bacteria were cultured on freshly prepared agar plates and incubated, lid uppermost, under microaerobic conditions at 37°C for 2-3 days. *E. coli* strains HB101 (Boyer and Roulland-Dussoix, 1969) and MC1061 (Maniatis et al., 1983), used in the cloning experiments, were grown routinely in Luria broth without glucose added or on Luria agar medium, at 37°C. Bacteria grown under nitrogen-limiting conditions were passaged on a nitrogen-limiting solid medium consisting of ammonium-free M9 minimal medium (pH 7.4) supplemented with 0.4% (w/v) D-glucose and 10 mM L-arginine (Cussac et al., 1992).

2. DNA manipulations:

All standard DNA manipulations and analyses, unless mentioned otherwise, were performed according to the procedures described by Maniatis et al. (1983).

3. Isolation of H. felis DNA:

Total genomic DNA was extracted by an sarkosyl-proteinase K lysis procedure (Labigne-Roussel et al., 1988). Twelve blood agar plates inoculated with *H. felis* were incubated in an anaerobic jar (BBL) with an anaerobic gaspak (BBL 70304) without catalyst, for 1-2 days at 37°C. The plates were harvested in 50 ml of a 15% (v/v) glycerol - 9% (w/v) sucrose solution and centrifuged at 5,000

rpm (in a Sorvall centrifuge), for 30 min at 4°C. The pellet was resuspended in 0.2 ml 50 mM D-glucose in 25 mM Tris-10 mM EDTA (pH 8.0) containing 5 mg ml^{-1} lysozyme and transferred to a VTi65 polyallomer quick seal tube. A 0.2 ml aliquot of 20 mg ml^{-1} proteinase K and 0.02 ml of 5M sodium perchlorate were added to the suspension. Cells were lysed by adding 0.65 ml of 0.5M EDTA - 10% (w/v) and incubated at 65°C until the suspension cleared (approximately). The volume of the tube was completed with a CsCl solution consisting (100 ml) of 126 g CsCl, 1 ml aprotinine, 99 ml TES buffer (30 mM Tris, 5 EDTA, 50 mM NaCl (pH 7.5). Lysates were centrifuged at 45,000 rpm, for 18°C. Total DNA was collected and dialyzed against TE buffer (10 mM Tris EDTA), at 4°C.

4. Cosmid cloning:

Chromosomal DNA from *H. felis* was cloned into cosmid vector pILL575, as previously described (Labigne et al., 1991). Briefly, DNA fragments arising from a partial digestion with *Sau*3A were sized on a (10 to 40%) sucrose density gradient and then ligated into a *Bam*HI-digested and dephosphorylated pILL575 DNA preparation. Cosmids were packaged into phage lambda particles (Amersham, In Vitro packaging kit) and used to infect *E. coli* HB101. To screen for urease expression, kanamycin-resistant transductants were replica-plated onto solid nitrogen-mimiting medium (see above) containing (20 μg ml^{-1}) kanamycin that had been dispensed into individual wells of microtitre plates (Becton Dickinson). The microtiter plates were incubated aerobically at 37°C for 2 days before adding 0.1 ml urease reagent (Hazell et al., 1987) to each of the wells. Ureolysis was detected within 5-6 h at 37°C by a color change in the reagent. Several urease-positive cosmid clones were restriction mapped and one was selected for subcloning.

5. Subcloning of H. felis DNA:

A large-scale CsCl plasmid preparation of cosmid DNA was partially digested *Sau*3A. DNA fragments (7 - 11 kb) were electroeluted from an agarose gel and purified using phenol-chloroform extractions. Following precipitation in cold ethanol, the fragments were ligated into Bg/III-digested plasmid pILL570 (Labigne et al., 1991) and the recombinant plasmids used to transform competent *E. coli* MC1061 cells. Spectinomycin-resistant transformants were selected and screened for urease expression under nitrogen-rich (Luria agar) and nitrogen-limiting conditions.

6. Quantitative urease activity:

Cultures grown aerobically for 2.5 days at 37°C were harvested and washed twice in 0.85% (w/v) NaCl. Pellets were resuspended in PEB buffer (0.1 M sodium phosphate buffer (pH 7.4) containing 0.01 M EDTA) and then sonicated by four 30-sec bursts using a Branson Sonifier Model 450 set at 30 W, 50% cycle. Cell debris was removed from the sonicates by centrifugation. Urease activities of the sonicates were measured in a 0.05 M urea solution prepared in PEB by a modification of the Berthelot reaction (Cussac et al., 1992). Urease activity was expressed as μmol urea $min^{-1}mg^{-1}$ bacterial protein.

7. Protein determination:

Protein concentrations were estimated with a commercial version of the Bradford assay (Sigma Chemicals).

8. Transposon mutagenesis:

Random insertional mutations were generated within cloned *H. felis* via a MiniTn3-Km delivery system (Labigne et al., 1992). In brief, *E. coli* HB101 cells containing the transposase-encoding plasmid pTCA were transformed with plasmid pILL570 containing cloned *H. felis* DNA. Transposition of the MiniTn3-Km element into the pILL570 derivative plasmids was effected via conjugation. The resulting cointegrates were then selected for resolved structures in the

presence of high concentrations of kanamycin (500 mg l^{-1}) and

(300 mg l^{-1}).

9. SDS-PAGE and Western Blotting:

Solubilized cell extracts were analyzed on slab gels, comprising a 4.5% acrylamide stacking gel and 12.5% resolving gel, according to the procedure of Laemmli (Laemmli, 1970). Electrophoresis was performed at 200V on a mini-slab gel apparatus (Bio-Rad).

Proteins were transferred to nitrocellulose paper (Towbin et al., 1979) in a Mini Trans-Blot transfer cell (Bio-Rad) set at 100 V for 1 h (with cooling). Nitrocellulose membranes were blocked with 5% (w/v) purified casein (BDH) in phosphate-buffered saline (PBS) at room temperature, for 2 h (Ferrero et al., 1992). Membranes were reacted at 4°C overnight with antisera diluted in 1% (w/v) casein prepared in PBS. Immunoreactants were then detected using a biotinylated secondary antibody (Kirkegaard and Perry Lab.) in combination with avidin-peroxidase (KPL). A substrate solution composed of 0.3% (w/v) 4-chloro-1-naphthol (Bio-Rad) was used to visualize reaction products.

10. DNA Sequencing:

DNA fragments to be sequenced were cloned into M13mp18 and M13mp19 (Meissing and Vieira, 1982) bacteriophage vectors (Pharmacia). Competent *E. coli* JM101 cells were transfected with recombinant phage DNA and plated on media containing X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside) and isopropyl-β-D-thiogalactopyranoside. Plaques arising from bacteria infected with recombinant phage DNA were selected for the preparation of single-stranded DNA templates by polyethylene glycol treatment (Sanger et al., 1977). Single-stranded DNA sequenced according to the dideoxynucleotide chain termination method using a Sequenase kit (United States Biochemical Corp.).

11. Nucleotide sequence accession number:

The nucleotide accession number is X69080 (EMBL Data Library).

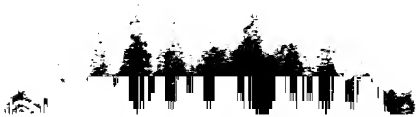
B. Results Of Part I Experiments:

1. Expression of urease activity by *H. felis* cosmid clones:

Cloning of partially digested fragments (30 to 45 kb in size) of *H. felis* chromosomal DNA into the cosmid vector pILL575 resulted in the isolation of approximately 700 cosmid clones. The clones were subcultured on nitrogen-limiting medium in order to induce urease expression (Cussac et al., 1992). Six of these were identified as being urease-positive after 5-6 h incubation (as described in the Experimental procedures section). No other urease-positive cosmid clones were identified, even after a further overnight incubation. Restriction enzyme analysis of 3 clones harboring the urease-encoding cosmids revealed a common 28 kd DNA fragment. A cosmid (designated pILL199) containing DNA regions at both extremities of the common fragment was selected for subcloning.

2. Identification of H. felis genes required for urease expression when cloned in *E. coli* cells:

To define the minimum DNA region necessary for urease expression in *E. coli* cells, the urease-encoding cosmid pILL199 was partially digested with *Sau*3A and the fragments were subcloned into plasmid pILL570. The transformants were subcultured on nitrogen-rich and nitrogen-limiting media and screened for an urease-positive phenotype. Five transformants expressed urease activity when grown under nitrogen-limiting conditions, whereas no activity was detected following growth on nitrogen-rich medium. Restriction mapping analyses indicated that the urease-encoding plasmids contained inserts of between 7 and 11 kb. The plasmid designated pILL205 was chosen for further studies.



Random mutagenesis of cloned *H. felis* DNA was performed to investigate putative regions essential for urease expression in *E. coli* and to localize the region of cloned DNA that contained the structural urease genes. Random insertion mutagenesis of prototype plasmid pILL205 were thus generated using the MiniTn3-Km element (Labigne et al., 1992). The site of insertion was restriction mapped for each of the mutated copies of pILL205 and cells harboring these plasmids were assessed qualitatively for urease activity (Fig. 1). A selection of *E. coli* HB101 cells harboring the mutated derivatives of pILL205 (designated "a" to "i") were then used both for quantitative urease activity determinations, as well as for the detection of the putative urease subunits by Western blotting.

The urease activity of *E. coli* HB101 cells harboring pILL205 was 1.2 ± 0.5 mmol urea $min^{-1}mg^{-1}$ bacterial protein (Table 1), which is approximately a fifth that of the parent *H. felis* strain used for the cloning. Insertion of the transposon at sites "a", "c", "d", "f" and "g" resulted in a negative phenotype, whilst mutations at sites "b", "e", "h" and "i" had no significant effect on the urease activities of clones harboring these mutated copies of pILL205 (Table 1). Thus mutagenesis of pILL205 with the MiniTn3-Km element identified three domains as being required for *H. felis* urease gene expression in *E. coli* cells.

3. Localization of the *H. felis* urease structural genes:

Western blot analysis of extracts of *E. coli* cells harboring pILL205 indicated the presence of two polypeptides of approximately 30 and 66 kDa, which cross-reacted with polyclonal *H. felis* rabbit antiserum (Fig. 2A). These proteins were not produced by bacteria carrying the vector (pILL570). Native *H. felis* urease has been reported to be composed of repeating monomeric subunits with calculated molecular weights of 30 and 69 kDa (Turbett et al., 1992). Thus, the 30 and 66 kDa proteins were thought to correspond to the *UreA* and *UreB* gene products, respectively. Interestingly an extract of *E. coli* cells harboring the recombinant plasmid pILL763 (Cussac et al., 1992) containing the *Helicobacter pylori UreA* and *UreB* genes, expressed two polypeptides with approximate molecular sizes of 30 and 62 kDa, which cross-reacted with the anti-*H. felis* antisera (Fig. 2B).

Table 1. Mutagensis of *E. coli* clones and effect on urease activity.

plasmids[a]	Urease activity[b] (mmol urea min^{-1} mg^{-1} protein)
pILL205	1.2 ± 0.46[c]
pILL205 :: a	neg[d]
pILL205 :: b	0.74 ± 0.32
pILL205 :: c	neg
pILL205 :: d	neg
pILL205 :: e	0.54 ± 0.15
pILL205 :: f	neg
pILL205 :: g	neg
pILL205 :: h	1.05 ± 0.25
pILL205 :: i	0.93 ± 0.35

a *E. coli* cells harbored pILL205 and its derivatives constructed by transposon mutagenesis. The letters correspond to the insertion sites of the MiniTn3-transposon on pILL205.

b Activities of bacteria grown aerobically for 3 days at 37°C on solid M9 minimal medium supplemented with 10 mM L-arginine. The values represent the means ± standard deviations calculated from three determinations.

c Urease activity was approximately a fifth as large as that of *H. felis* wild-type strain (ATCC 49179), *i.e.* 5.7 ± 0.1 mmol urea min^{-1} protein (Ferrero and Lee, 1991).

d No activity detected (limit of detection was < 1 nmol urea min^{-1} mg^{-1} of bacterial protein).

Clones harboring the mutated derivatives of pILL205, in all but one case, expressed the *UreA* and *UreB* gene products (Figs. 2A, B). Given that several of the mutants (i.e., mutants "c", "d", "f" and "g") synthesized the urease subunits yet did not produce an active enzyme, it is possible to speculate that accessory functions essential for urease activity may have been disrupted by transposon insertion. In contrast, the mutant designated pILL205::a did not produce the *UreB* product and was urease-negative. Thus, the site of transposon insertion was presumed to be located in the *UreB* gene. Sequence analyses of the DNA region corresponding to insertion site "a" were undertaken to elucidate potential open reading frames encoding the structural polypeptides of *H. felis* urease.

4. Sequence analyses of *H. felis* structural urease genes:

Sequencing of a 2.4 kb region of *H. felis* DNA adjacent to transposon insertion site "a" resulted in the identification of two open reading frames (ORFs) designated *UreA* and *UreB*, which are transcribed in the same direction (Fig. 3). The transposon was confirmed to be located at 240 bp upstream from the end of *UreB*. Both ORFs commenced with an ATG start codon and were preceded by a site similar to the *E. coli* consensus ribozome-binding sequence (Shine and Dalgarno, 1974). The intergenic space for the *H. felis* structural genes consisted of three codons, which were in phase with the adjacent open reading frames. This suggests that, as has already been observed to be the case for *Helicobacter pylori* (Labigne et al., 1991), a single mutation in the stop codon of the *ure A* gene would theoretically result in a fused single polypeptide.

The *H. felis UreA* and *UreB* genes encode polypeptides with calculated molecular weights of 26,074 Da and 61,663 Da, respectively, which are highly

homologous at the amino acid sequence level to the *UreA* and *UreB* gene products of *H. pylori*. The levels of identity between the corresponding *ure A* and *ure B* gene products of the two *Helicobacter* spp. was calculated to be 73.5% and 88.2%, respectively. From the amino acid sequence information, the predicted molecular weights of the *UreA* and *UreB* polypeptides from *H. felis* and *H. pylori* (Labigne et al., 1991) are very similar. Nevertheless the *UreB* product of *H. felis* had a lower mobility than the corresponding gene product from *Helicobacter pylori* when subjected to SDS-polyacrylamide gel electrophoresis (Fig. 2B)

II. Expression of Recombinant Urease Subunit Proteins From *H. Pylori* and *H. Felis*: Assessment of These Proteins as Potential Mucosal Immunogens in a Mouse Model:

The aims of the study were to develop recombinant antigens derived from the urease subunits of *H. pylori* and *H. felis*, and to assess the immunoprotective efficacies of these antigens in the *H. felis*/mouse model. Each of the structural genes encoding the respective urease subunits from *H. pylori* and *H. felis* was independently cloned and over-expressed in *Escherichia coli*. The resulting recombinant urease antigens (which were fused to a 42 kDa maltose-binding protein of *E. coli*) were purified in large quantities from *E. coli* cultures and were immunogenic, yet enzymatically inactive. The findings demonstrated the feasibility of developing a recombinant vaccine against *H. pylori* infection.

A. Experimental Procedures For Part II:

1. Bacterial strains, plasmids and growth conditions:

H. felis (ATCC 49179) was grown on a blood agar medium containing blood agar base no. 2 (Oxoid) supplemented with 10% lysed horse blood

(BioMérieux) and an antibiotic supplement consisting of vancomycin (10 μg/mL), polymyxin B (25 ng/mL), trimethoprim (5 μg/mL) and amphotericin B (25 μg/mL). Bacteria were cultured under microaerobic conditions at 37° C for 2 days, as described previously. *E. coli* strains MC1061 and JM101, used in cloning and expression experiments, were grown routinely at 37° C in Luria medium, with or without agar added. The antibiotics carbenicillin (100 μg/mL) and spectinomycin (100 μg/mL) were added as required.

2. DNA manipulations and analysis:

All DNA manipulations and analyses, unless mentioned otherwise, were performed according to standard procedures. Restriction and modification enzymes were purchased from Amersham (France). DNA fragments to be cloned were electroeluted from agarose gels and then purified by passage on Elutip mini-columns (Schleicher and Schull, Germany). Single-stranded DNA sequencing was performed using M13mp18 and M13mp19 bacteriophage vectors (Pharmacia, France). Single-stranded DNA templates were prepared from recombinant phage DNA by polyethylene glycol treatment. Sequencing of the templates was achieved according to the dideoxynucleotide chain termination method using a Sequenase kit (United States Biochemical Corp., U.S.A.).

3. Preparation of inserts for cloning using the polymerase chain reaction (PCR):

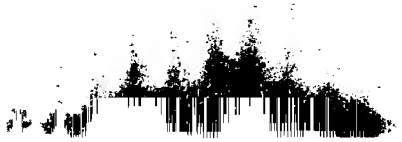
To clone the *UreA* genes of *H. pylori* and *H. felis*, degenerate 36-mer primers were conceived from the published urease sequences (Labigne et al., 1991; Ferrero and Labigne, 1993) (primer set #1; refer to Table 2). Purified DNA from *E. coli* clones harboring plasmids pILL763 and pILL207 (Table 3), that encoded the structural genes of *H. pylori* and *H. felis* ureases, were used as template material in PCR reactions. Reaction samples contained: 10 - 50 ng of denatured DNA; PCR buffer (50 mmol/L KC1 in 10 mmol/L Tris-HCl [pH 8.3)]); dATP, dGTP, dCTP and dTTP (each at a final concentration of 1.25 mmol/L); 2.5

mmol/L $MgCl_2$; 25 pmol of each primer and 0.5 µL *Taq* polymerase. The samples were subjected to 30 cycles of the following program: 2 min at 94° C, 1 min at 40° C.

The amplification products were cloned into the cohesive ends of the pAMP vector (Fig. 1) according to the protocol described by the manufacturer ("CloneAmp System", Gibco BRL; Cergy Pontoise, France). Briefly, 60 ng of amplification product was directly mixed in a buffer (consisting of 50 mmol/L KCl, 1.5 mmol/L $MgCl_2$, 0.1% (wt/vol) gelatine in 10 mmol/L Tris-HCl, pH 8.3) with 50 ng of the pAMP 1 vector DNA and 1 unit of uracil DNA glycolsylase. Ligation was performed for 30 min at 37° C. Competent cells (200 µL) of *E. coli* MC1061 were transformed with 20 µL of the ligation mixture. Inserts were subsequently excised from the polylinker of the pAMP vector by double digestion with *Bam*HI and *Pst*1, and then subcloned into the expression vector pMAL (New England Biolabs Inc., Beverly, USA) chosen for the production of recombinant antigens (pILL919 and pILL920, respectively, Fig. 13), as well as in M13mp bacteriophage for sequencing.

Amplification of a product containing the *UreB* gene of *H. pylori* was obtained by PCR using a couple of 35-mer primers (set #2, Table 2). The PCR reaction mixtures were first denatured for 3 min at 94° C, then subjected to 30 cycles of the following program: 1 min at 94° C, 1 min at 55° C, and 2 min at 72° C. The purified amplification product (1850 bp was digested with *Eco*RI and *Pst*I and then cloned into pMAL (pILL927, Fig. 2). Competent cells of *E. coli* MC1061 were transformed with the ligation reaction.

H. felis UreB was cloned in a two-step procedure that allowed the production of both complete and truncated versions of the UreB subunit. Plasmid pILL213 (Table 3) was digested with the enzymes *Dra*I, corresponding to amino acid residue number 219 of the UreB subunit and *Hind*III. The resulting 1350 bp fragment was purified and cloned into pMAL that had been digested with *Xmn*I



and *Hind*III (pILL219, Fig. 2). In order to produce a clone capable of synthesizing a complete UreB protein, PCR primers were developed (set #3, Table 2) that amplified a 685 bp fragment from the N-terminal portion of the *ureB* gene (excluding the ATG codon), that also overlapped the beginning of the insert in plasmid pILL219. The PCR amplified material was purified and digested with *bam*HI and *Hind*III, and then cloned into pMAL (pILL221, Figure 14). A 1350 bp *Pst*I-*Pst*I fragment encoding the remaining portion of the UreB gene product was subsequently excised from pILL219 and cloned into a linearized preparation of pILL221 (pILL222, Fig. 14).

4. Expression of recombinant urease polypeptides in the vector pMAL:

The expression vector pMAL is under the control of an inducible promoter (P_{lac}) and contains an open-reading frame (ORF) that encodes the production of MalE (Maltose-binding protein, MBP). Sequences cloned in-phase with the latter ORF resulted in the synthesis of MBP-fused proteins, which were easily purified on amylose resin. Of the two versions of pMAL that are commercially available, the version not encoding a signal sequence (*i.e.*, pMAL-c2) synthesized greater amounts of recombinant proteins and was thus used throughout.

E. coli clones harboring recombinant plasmids were screened for the production of fusion proteins prior to performing large-scale purification experiments.

5. Purification of recombinant urease polypeptides:

Fresh 500 mL volumes of Luria broth containing carbenicillin (100 μg/mL and 2% (wt/vol) glucose were inoculated with overnight cultures (5 mL) of *E. coli* clones. The cultures were incubated at 37° C and shaken at 250 rpm, until the A_{600} = 0.5. Prior to adding 1 mmol/L (final concentration) isopropyl-β-D-thiogalacto-pyranoside (IPTG) to cultures, a 1.0 mL sample was taken (non-

induced cells). Cultures were incubated for a further 4 h at which time another 1.0 mL sample (induced cells) was taken. The non-induced and induced cell samples were later analyzed by SDS-PAGE.

IPTG-induced cultures were centrifuged at 7000 rpm for 20 min at 4° C and the supernatant discarded. Pellets were resuspended in 50 mL column buffer (200 mmol/L NaCl, 1 mmol/L EDTA in 10 mmol/L Tris HCl,pH 7.4), containing the following protease inhibitors (supplied by Boehringer, Mannheim, Germany): 2 µmol/L leupeptin, 2 µmol/L pepstatin, and 1 mmol/L phenylmethylsulphonyl fluoride (PMSF). Intact cells were lysed by passage through a French Pressure cell (16,000 lb/in^2). Cell debris was removed by centrifugation and lysates were diluted in column buffer to give a final concentration of 2.5 mg protein/mL, prior to chromatography on a 2.6 cm x 20 cm column of amylose resin (New England Biolabs). The resin was washed with column buffer at 0.5 mL/min until the A_{280} returned levels. The MBP-fused recombinant proteins were eluted from the column by washing with column buffer containing 10 mmol/L *p-maltose*.

Fractions containing the recombinant proteins were pooled and then dialyzed several times at 4 C against a low salt buffer (containing 25 mmol/L NaCl in 20 mmol/L TrisHCl, pH 8.0). The pooled fractions were then loaded at a flow rate of 0.5 mL/min onto a 1.6 x 10 cm anion exchange column (HP-Sepharose, Pharmacia, Sweden) connected to a Hi-Load chromatography system (Pharmacia). Proteins were eluted from the column using a salt gradient (25 mmol/L to 500 mmol/L NaCl). Fractions giving high absorbance readings at A_{280} were exhaustively dialyzed against distilled water at 4° C and analyzed by SDS-PAGE.

6. Rabbit antisera:

Polyclonal rabbit antisera was prepared against total cell extracts of *H. pylori* strain 85P (Labigne et al., 1991) and *H. felis* (ATCC 49179). Polyclonal

rabbit antisera against recombinant protein preparations of *H. pylori* and *H. felis* urease subunits was produced by immunizing rabbits with 100 mg of purified recombinant protein in Freund's complete adjuvant (Sigma). Four weeks later, rabbits were booster-immunized with 100 µg protein in Freund's incomplete adjuvant. On week 6, the animals were terminally bled and the sera kept at -20° C.

7. Protein analyzes by SDS-PAGE and Western blotting:

Solubilized cell extracts were analyzed on slab gels comprising a 4.5% acrylamide stacking gel and a 10% resolving gel, according to the procedure of Laemmli. Electrophoresis was performed at 200 V on a mini-slab gel apparatus (Bio-Rad, USA).

Proteins were transferred to nitrocellulose paper in a Mini Trans-Blot transfer cell (Bio-Rad) set at 100 V for 1 h, with cooling. Nitrocellulose membranes were blocked with 5% (wt/vol) casein (BDH, England) in phosphate-buffered saline (PBS, pH 7.4) with gentle shaking at room temperature for 2 h. Membranes were reacted at 4° C overnight with antisera diluted in 1% casein prepared in PBS. Immunoreactants were detected using specific biotinylated secondary antibodies and streptavidin-peroxidase conjugate (Kirkegaard and Parry Lab., Gaithersburg, USA). Reaction products were visualized on autoradiographic film (Hyperfilm, Amersham, France) using a chemiluminescence technique (ECL system, Amersham).

Protein concentrations were determined by the Bradford assay (Sigma Chemicals corp., St Louis, USA).

8. Animal experimentation:

Six week old female Swiss Specific Pathogen-Free (SPF) mice were obtained (Centre d'Elevage R. Janvier, Le-Genest-St.-Isle, France) and maintained on a commercial pellet diet with water *ad libitum*. The intestines of

the animals were screened for the absence of *Helicobacter muridarum*. For all orogastric administrations, 100 µL aliquots were delivered to mice using 1.0 mL disposable syringes to which polyethylene catheters (Biotrol, Paris, France) were attached.

9. Preparation of sonicated extracts and inocula from *H. felis* cultures:

H. felis bacteria were suspended in PBS and centrifuged at 5000 rpm, for 10 min in a Sorvall RC-5 centrifuge (Sorvall, USA) at 4° C. The pellets were washed twice and resuspended in PBS. Bacterial suspensions were sonicated as previously described and were subjected to at least one freeze-thaw cycle. Protein determinations were carried out on the sonicates.

To ensure a virulent culture of *H. felis* for protection studies, *H. felis* bacteria were maintained *in vivo* until required. Briefly, mice were inoculated three times (with 10^{10} bacteria/mL), over a period of 5 days. The bacteria were reisolated from stomach biopsies on blood agar medium (4 - 7 days' incubation in a microaerobic atmosphere at 37° C). Bacteria grown for two days on blood agar plates were harvested directly in peptone water (Difco, USA). Bacterial viability and motility were assessed by phase microscopy prior to administration to animals.

10. Mouse proton studies:

Fifty mg of recombinant antigen and 10 µg cholera holotoxin (Sigma Chemical Corp.), both resuspended in HCO_3, were administrated orogastrically to mice on weeks 0, 1, 2 and 3. Mice immunized with sonicated *H. felis* extracts (containing 400 - 800 µg of total protein) were also given 10 µg of cholera toxin. On week 5, half of the mice from each group were challenged with an inoculum of virulent *H. felis*. The remainder of the mice received an additional "boost" immunization on week 15. On week 17 the latter were challenged with a culture of *H. felis*.

11. Assessment of *H. felis* colonization of the mouse:

Two weeks after receiving the challenge dose (*i.e.*, weeks 7 and 19, respectively) mice were sacrificed by spinal dislocation. The stomachs were washed twice in sterile 0.8% NaCl and a portion of the gastric antrum from each stomach was placed on the surfaces of 12 cm x 12 cm agar plates containing a urea indicator medium (2% urea, 120 mg Na_2HPO_4, 80 mg KH_2PO_4, 1.2 mg phenol red, 1.5 g agar prepared in 100 mL). The remainder of each stomach was placed in formal-saline and stored until processed for histology. Longitudinal sections (4 μm) of the stomachs were cut and routinely stained by the Giemsa technique. When necessary, sections were additionally stained by the Haematoxylin-Eosin and Warthin-Starry silver stain techniques.

The presence of *H. felis* bacteria in mouse gastric mucosa was assessed by the detection of urease activity (for up to 24 h) on the indicator medium, as well as by the screening of Giemsa-stained gastric sections that had been coded so as to eliminate observer bias. The numbers of bacteria in gastric sections were semi-quantitatively scored according to the following scheme: 0, no bacteria seen throughout sections; 1, few bacteria (< 20) seen throughout; 2, occasional high power (H.P.) field with low numbers (< 20) of bacteria; 3, occasional H.P. field with low to moderate numbers (< 50) of bacteria; and 4, numerous (> 5) H.P. fields with high numbers of bacteria (> 50). Mononuclear cell infiltrates were scored as follows: 0, no significant infiltration; 1, infiltration of low numbers of mononuclear cells limited to the submucosa and muscularis mucosa; 2, infiltration of moderate numbers of mononuclear cells to the submucosa and muscularis mucosa, sometimes forming loose aggregates; and 3, infiltration of large numbers of mononuclear cells and featuring nodular agglomerations of cells.

B. Results Of Part II Experiments:

1. Expression of *Helicobacter* urease polypeptides in *E. coli*:

Frag[illegible] containing the sequences encoding the respective *UreA* gene products of *H. fe[illegible]pylori* were amplified by PCR and cloned in-phase with an ORF encoding the 42 kDa MBP, present on the expression vector pMAL. Sequencing of the PCR products revealed minor nucleotide changes that did not, however, alter the deduced amino acid sequences of the respective gene products. *E. coli* MC1061 cells transformed with these recombinant plasmids (pILL919 and pILL920, respectively) expressed fusion proteins with predicted molecular weights of approximately 68 kDa. Following chromatography on affinity (amylose resin) and anion exchange gel media (Q-Sepharose), these proteins were purified to high degrees of purity (Fig. 1). The yield from 2-L cultures of recombinant *E. coli* cells was approximately 40 mg of purified antigen.

Similarly, the large UreB subunits of *H. pylori* and *H. felis* ureases were expressed in *E. coli* (plasmids pILL927 and pILL222, respectively) and produced fusion proteins with predicted molecular weights of 103 kDa. The yield in these cases was appreciably lower than for the UreA preparations (approximately 20 mg was recovered from 2-L of bacterial culture). Moreover, problems associated with the cleavage of the UreB polypeptides from the MBP portion of the fusion proteins were encountered. These difficulties were attributed to the large sizes of the recombinant UreB polypeptides.

2. Analysis of the recombinant urease polypeptides:

Western blot analyses of the antigen preparations with rabbit polyclonal antisera raised to whole-extracts of *H. pylori* and *H. felis* bacteria demonstrated that the antigens retained immunogenicity to the homologous as well as heterologous antisera (Figs. 14 and 15). The antisera did not recognize the MBP

component alone. Cross-reactivity between the urease polypeptides of *H. pylori* and *H. felis* was consistent with the high degrees of identity between the amino acid sequences of these proteins.

Rabbit polyclonal antisera raised against purified recombinant UreA and UreB proteins prepared from *H. pylori* and *H. felis* strongly reacted with the urease polypeptides present in whole-cell extracts of the bacteria (Fig. 16). As we had already observed, the UreB subunit of *H. felis* urease migrated slightly higher on SDS-PAGE gels than did that of *H. pylori* (Fig. 16).

3. Preparation of *H. felis* inocula used in immunoprotection studies:

To ensure the virulence of *H. felis* bacterial inocula, bacteria were reisolated from *H. felis*-infected mouse stomachs (see Materials and Methods). The bacteria were passaged a minimum number of times *in vitro*. Stock cultures prepared from these bacteria, and stored at -80° C, were used to prepare fresh inocula for other mouse protection studies. This procedure ensured that the inocula used in successive experiments were reproducible.

Immunization of mice against gastric *H. felis* infection:

Mice that had been immunized for three weeks with the given antigen preparations were divided into two lots and one half of these were challenged two weeks later with an *H. felis* inoculum containing 10^7 bacteria/mL. One group of animals that had been immunized with recombinant *H. felis* UreA were also challenged but, unlike the other animals, were not sacrificed until week 19.

a) Protection at week 5:

Eighty-five % of stomach biopsy samples from the control group of mice immunized with *H. felis* sonicate preparations were urease-negative and therefore appeared to have been protected from *H. felis* infection (Table 4). This compared to 20% of those from the other control group of animals given MBP alone. The proportion of urease-negative stomachs for those groups of mice

given the recombinant urease subunits varied from 70% (for *H. pylori* UreB) to 20% (for *H. pylori* UreA).

The levels of bacterial colonization by *H. felis* was also assessed from coded histological slides prepared from gastric tissue. Due to the striking helical morphology of *H. felis* bacteria, the organisms could be readily seen on the mucosal surfaces of both gastric pit and glandular regions of the stomach. Histological evidence indicated that the levels of protection in mice was lower than that observed by the biopsy urease test: 25% and 20% of gastric tissue from mice immunized with *H. felis* sonicate preparations of *H. pylori* UreB, respectively, were free of *H. felis* bacteria.

Amongst certain groups of these mice the preponderance of urease-negative biopsies, as well as lower histological scores for bacterial colonization (unpublished data), suggested that an immunoprotective response had been elicited in the animals. This response, however, may have been insufficient to protect against the inoculum administered during the challenge procedure.

b) Protection at week 17:

The remaining mice, from each group of animals, were boosted on week 15. These mice were challenged at week 17 with an *H. felis* inoculum containing approximately 100-fold less bacteria than that used previously. Two weeks later all stomach biopsies from the MBP-immunized mice were urease-positive (Table 4). In contrast, urease activity for gastric biopsies from mice immunized with the recombinant urease subunits varied from 50% for *H. pylori* UreA to 100% for *H. felis* UreB. The latter was comparable to the level of protection observed for the group of animals immunized with *H. felis* sonicated extracts. Histological evidence demonstrated that the UreB subunits of *H. felis* and *H. pylori* protected 60% and 25% of immunized animals, respectively. This compared with a level of 85% protection for mice immunized with *H. felis* sonicated extracts. Immunization of mice with recombinant *H. pylori* UreA did not

protect the animals. Similarly, the stomachs of all *H. felis* UreA-immunized mice, that had been challenged at week 5, were heavily colonized with *H. felis* bacteria at week 19 (Table 4).

The urease gastric biopsy test, when compared to histological analysis of gastric tissue sections, gave sensitivity and specificity values of 63% and 95%, respectively. Thus, histology proved to be the more accurate predictor of *H. felis* infection in the mouse.

5. Cellular immune response in immunized stomachs:

In addition to the histological assessment of *H. felis* colonization, mouse gastric tissue was also scored (from 0 to 3) for the presence of a mononuclear cell response. In mice immunized with MBP alone, a mild chronic gastritis was seen with small numbers of mononuclear cells restricted to the muscularis mucosa and to the submucosa of the gastric epithelium. In contrast, there were considerable numbers of mononuclear cells present in the gastric mucosae from animals immunized with either the recombinant urease polypeptides, or with *H. felis* sonicate preparations. These inflammatory cells coalesced to form either loose aggregates, in the submucosal regions of the tissue, or nodular structures that extended into the mucosal regions of the gastric epithelia. The mononuclear cell response did not appear to be related to the presence of bacteria as the gastric mucosae from the *H. felis* UreA-immunized mice, that were heavily colonized with *H. felis* bacteria, contained little or no mononuclear cells.

Table 2. The oligomeric primers used in PCR-based amplification of urease-encoding nucleotide sequences.

Primer set	Nucleotide sequence (5' ->3')
#1 forw	...CAU CCT$^{\cdot}$ AAA^{G} GAA^{G} T^{C}TA$^{\cdot}$ GAT^{C} AAA^{G} T^{C}TA$^{\cdot}$ ATG
rev	T^{C}TC C^{T}TT A$^{\cdot}$CG A$^{\cdot}$CG A$^{\cdot}$G^{C}A^{T} A^{G,T}AT C^{T}TT C^{T}TT CAT CUA...
#2 forw	CC GGA GAA TTC ATT AGC AGA AAA GAA TAT GTT TCT ATG *Eco*RI¥
rev	AC GTT CTG CAG CTT ACG AAT AAC TTT TGT TGC TTG AGC *PstI*¥
#3 forw	GGA TCC AAA AAG ATT TCA CG *Bam*HI¥
rev	GGA AGC TT C TGC AGG TGT GCT TCC CCA GTC *Hind*III¥ *PstI*¥

* Degenerated nucleotides in which all possible permutations of the genetic code were included (A, T, G, C).

G,C,T The given nucleotides were degenerate with the specific base(s) shown.

¥ Restriction sites introduced in the amplified fragments.

Table 3. Plasmids used.

Plasmid	Vector	Relevant phenotype or character	Reference
pILL763	pILL570	9.5 kb fragment (Sau3a partial digest of H. pylori chromosome)(Sp^R)	Cussac et al., 1991
pILL199	pILL575	35 kb fragment (Sau3A partial digest of H. felis chromosome)	Ferrero & Labigne, '93
pILL207	pILL570	11 kb fragment (Sau3A partial digest of pILL199)	Infection & Immunity 1994, 62: 4981-4989
pILL919	pMAL-C2	0.8 kb BamHI-PstI[a] insert containing a nucleotide fragment encoding H.felis ureA gene (Ap^R)	Infection & Immunity 1994, 62: 4981-4989

Plasmid	Vector	Relevant phenotype or character	Reference
pILL920	pMAL-C2	0.8 kb BAMHI-PstI[a] insert containing PCR product encoding H. pylori ureA gene	Infection & Immunity 1994, 2: 4981-4989
pILL927	pMAL-C2	1.8 kb EcoRI-PstIa PCR fragment encoding H. pylori ureB gene	Infection & Immunity 1994, 62: 4981-4989
pILL213	pUC19	2 kb fragment resulting from Sau2A partial digest of pILL207 (Ap^R)	Infection & Immunity 1994, 62: 4981-4989
pILL219	pMAL-C2	1.4 kb DraI-HindIII[b] insert containing H. felis ureB (bases 657 - 1707)	Infection & Immunity 1994, 62: 4981-4989

Plasmid	Vector	Relevant phenotype or character	Reference
pILL221	pMAL-C2	0.7 kb BamHI-PstI PCR fragment encoding H. felis ureB (bases 4 - 667)	Infection & Immunity 1994, 62: 4981-4989
pILL222	pMAL-C2	1.35 kb PstI-PstI fragment encoding H. felis ureN (bases 667 - 1707) from pILL219 cloned into linerized pILL221	Infection & Immunity 1994, 62: 4981-4989

Table 4. Protection of mice by immunization with recombinant urease proteins.

Antigen	Protection (%)a			
	Urease		Histology	
MBP	0 %	(0/10)	0 %	(0/10)
UreA *H. pylori*	50	(4/8)	0	(0/10)
UreA *H. felis*[b]	12.5	(1/8)	0	(0/10)
UreB *H. pylori*	65	(5/8)	25	(2/8)
UreB *H. felis*	100	(7/7)	60	(5/7)
H. felis sonicate	100	(8/8)	85	(7/8)

a Challenge inoculum dose was 10^5 bacteria/mouse

b Mice were challenged on week 5 (with 10^7 bacteria) and were sacrificed on week 19.

III. *Helicobacter Pylori HspAB* Heat Shock Gene Cluster: Nucleotide Sequence, Expression And Function:

A homolog of the heat shock proteins (Hsps) of the GroEL class, reported to be closely associated with the virulence of *Helicobacter pylori* (a nickel metalloenzyme), has recently been purified from *H. pylori* cells by Dunn et al., and Evans et al. (Infect. Immun. 60:1946, 1952, 1946 and 2125, respectively). Based on the reported N-terminal amino acid sequence of this immunodominant protein, degenerate oligonucleotides were synthesized in order to target the gene (*hspB*) encoding the GroEL-like protein in the chromosome of *H. pylori* strain 85P. Following gene amplification, a 108-base pair (bp)-fragment encoding the 36 first amino acids of the *hspB* protein was purified, and used a probe to identify in the *H. pylori* genomic bank a recombinant cosmid harboring the entire *hspB* encoding gene. The *hspB* gene was mapped to a 3.15 kilobases (kb) *Bgl*II restriction fragment of the pILL684 cosmid (Table 5). The nucleotide sequence of that fragment subcloned into the pILL570 plasmid vector (pILL689) revealed the presence of two open reading frames (OFRs) designated *hspA* and *hspB*, the organization of which was very similar to be groESL bicistronic operons of other bacterial species. *hspA* and *hspB* encode polypeptides of 118 and 545 amino acids, respectively, corresponding to calculated molecular masses of 13.0 and 58.2 kilodaltons (kDa), respectively. Amino acid sequence comparison studies revealed i) that the *H. pylori* HspA and HspB protein were highly similar to their bacterial homologs; ii) that the HspA *H. pylori* protein features a striking motif at the carboxyl terminus that other bacterial GroEs-homologs lack; this unique motif consists of a series of eight histidine residues resembling metal binding domain, such a nickel binding. Surprisingly, immediately upstream of the gene cluster an IS5 insertion element was found that was absent in the *H. pylori* genome, and was positively selected during the cosmid cloning process. The IS5 was found to be involved in the expression of the *hspA* and *hspB* genes in pILL689. The

expression of the HspA and HspB proteins from the pILL689 plasmid was analyzed in minicell-producing strain. Both polypeptides were shown to be constitutively expressed in the *E. coli* cells. When the pILL689 recombinant plasmid was introduced together with the *H. pylori* urease gene cluster into an *E. coli* host strain, an increase of urease activity was observed suggesting a close interaction between the heat shock proteins and the urease enzyme. Supporting the concept of a specific function for the HspA chaperone, was the fact that whereas a single *hspB* copy was found in the *H. pylori* genome, two copies of the *hspA* were found in the genome, one linked to the *hspB* gene and one unlinked to the *hspB* gene. Attempts to construct isogenic mutants of *H. pylori* in the *HspA* and the *hspB* gene were unsuccessful suggesting that these genes are essential for the survival of the bacteria.

A. Experimental Procedures For Part III:

1. Bacterial strains, plasmids, and culture conditions:

The cloning experiments were performed with genomic DNA prepared from *H. pylori* strain *H. pylori* strain N6 deposited at NCIMB No. 40512 on June 26, 1992 was used as the recipient strain for the electroporation experiments because of its favorable transformability. *E. coli* strain HB101 or strain MC1061 were used as a host for cosmid cloning and subcloning experiments, respectively. *E. coli* P678-54 was used for preparation of minicells. Vectors and recombinant plasmids used in this study are listed in Table 1. *H. pylori* strains were grown on horse blood agar plates, supplemented with vancomycin (10 mg/l), polymyxin B (2,500 U/l), trimethoprim (5 mg/l), and amphotericin B (4 mg/l). Plates were incubated at 37°C under microaerobic conditions in an anaerobic jar with a carbon dioxide generator envelope (BBL 70304). *E. coli* strains were grown in L-broth without glucose (10 g of tryptone, 5 g of yeast extract, and 5 g of NaCl per liter; pH 7.0) or on L-agar plates (1.5% agar) at 37°C. For measurement of urease activity, the nitrogen-limiting medium used consisted of ammonium-free M9 minimal agar medium (pH 7.4) containing 0.4% D-glucose as the carbon source, and freshly prepared filter-sterilized L-arginine added to the final concentration of 10 mM. Antibiotic concentrations for the selection of recombinant clones were as follows (in milligrams per liter): kanamycin, 20; spectinomycin, 100; carbenicillin, 100.

2. Preparation of DNA:

Genomic DNA from *H. pylori* was prepared as previously described. Cosmid and plasmid DNAs were prepared by an alkaline lysis procedure followed by purification in cesium chloride-ethidium bromide gradients as previously described.

3. Cosmid cloning:

The construction of the cosmid gene bank of *H. pylori* 85P in *E. coli* HB101, which was used for the cloning of the *H. pylori HspA-B* gene cluster, has been described previously. Labigne et al., 1991, J. Bact. 173:1920.

4. DNA analysis and cloning methodology:

Restriction endonucleases, T4 DNA ligase, DNA polymerase I large (Klenow) fragment, and *Taq* polymerase were purchased from Amersham, T4 DNA polymerase from Biolabs, and calf intestinal phosphatase from Pharmacia. All enzymes were used according to the instructions of the manufacturers. DNA fragments were separated on agarose gels run in Tris-acetate buffer. The 1-kb ladder from Bethesda Research Laboratories was used as a fragment size standard. When necessary, DNA fragments were isolated by electroelution from agarose gels as previously described and recovered from the migration buffer by means of an Elutip-d minicolumn (Schleicher and Schuell, Dassel, Germany). Basic DNA manipulations were performed according to the protocols described by Sambrook et al.

5. Hybridization:

Colony blots for screening of the *H. pylori* cosmid bank and for identification of subclones were prepared on nitrocellulose membranes (Schleicher and Schuell, Dassel, Germany) according to the protocol of Sambrook et al. Radioactive labelling of PCR-products was performed by random priming using as primers the random hexamers from Pharmacia. Colony hybridizations were performed under high stringency conditions (5 x SSC, 0.1% SDS, 50% formamide, 42° C) (1 x SSC; 150 mM NaCl, 15 mM sodium citrate, pH 7.0). For Southern blot hybridizations, DNA fragments were transferred from agarose gels to nitrocellulose sheets (0.45 - µm pore size; Schleicher & Schuell, Inc.), and hybridized under low stringency conditions (5 x SSC, 0.1% SDS, 30 or

40% formamide, at 42° C with ^{32}P-labeled deoxyribonucleotide probes.) Hybridization was revealed by autoradiography using Amersham Hyperfilm-MP.

6. DNA sequencing:

Appropriate fragments of plasmid DNA were subcloned into M13 mp 18/19 vectors. Single-stranded DNA was prepared by phage infection of *E. coli* strain JM101. Sequencing was performed by the dideoxynucleotide chain termination method using the United States Biochemicals Sequenase kit. Both the M13 universal primer and additional specific primers (Fig. 1) were used to sequence both the coding and non-coding DNA strands. Sequencing of double-stranded DNA was performed as previously described. Direct sequencing of PCR product was carried out following purification of the amplified, electroeluted PCR product through an Elutip-d minicolumn (Schleicher & Schuell). The classical protocol for sequencing using the Sequenase kit was then used with the following modifications: PCR product was denatured by boiling annealing mixture containing 200 picomoles of the oligonucleotide used as primer and DMSO to the final concentration of 1% for 3 minutes; the mixture was then immediately cooled on ice; the labeling step was performed in presence of manganese ions (mM).

7. Electroporation of *H. pylori*:

In the attempt to construct *H. pylori* mutants, appropriate plasmid constructions carrying the targeted gene disrupted by a cassette containing a kanamycin resistance gene (*aph*3'-III), were transformed into *H. pylori* strain N6 by means of electroporation as previously described. Plasmid pSUS10 harboring the kanamycin disrupted *fla*A gene was used as positive control of electroporation. After electroporation, bacteria were grown on non-selective plates for a period of 48 h in order to allow for the expression of the antibiotic resistance and then transferred onto kanamycin-containing plates. The selective plates were incubated for up to 6 days.

8. Polymerase chain reaction (PCR):

PCRs were carried out using a Perkin-Elmer Cetus thermal cycler using the GeneAmp kit (Perkin-Elmer Cetus). Classical amplification reaction involved 50 picomoles (pmoles) of each primer and at least 5 pmoles of the target DNA. The target DNA was heat denatured prior to addition to the amplification reaction. Reaction consisted of 25 cycles of the following three steps: denaturation (94° C for 1 minute), annealing (at temperatures ranging between 42° and 55° C, depending on the calculated melting temperatures of the primers, for 2 min), and extension (72° C for 2 min). When degenerate oligonucleotides were used in nonstringent conditions, up to 1000 pmoles of each oligonucleotide were added, 50 cycles were carried out, and annealing was performed at 42° C.

9. Analysis of proteins expressed in minicells:

Minicells harboring the appropriate hybrid plasmid were isolated and labeled with [^{35}S] methionine (50 μ-m Ci/ml). Approximately 100,000 cpm of acetone-precipiTable material was subjected to sodium dodecyl sulfate (SDS)-polyacrylamide gel electrophoresis in a 12.5% gel. Standard proteins with molecular weights ranging from 94,000 to 14,000 (low< molecular-weights kit from Bio-Rad Laboratories) were run in parallel. The gel was stained and examined by fluorography, using En^{3}Hance (New England Nuclear).

10. Urease activity:

Urease activity was quantitated by the Berthelot reaction by using a modification of the procedure, which has already been described (Cussac et al., 1992, J. Bact. 176:2666-2673). Urease activity was expressed as micromoles of urea hydrolyzed per minute per milligram of bacterial protein.

B. Results Of Part III Experiments:

1. Identification of a recombinant cosmid harboring the *Helicobacter pylori* GroEL-like heat shock protein encoding gene:

Based on the published N-terminal amino sequence of the purified heat shock protein of *H. pylori*, two degenerate oligonucleotides were synthesized to target the gene of interest in the chromosome of *H. pylori* strain 85P. The first one 5' - **G C N A A R G A R A T H A A R T T Y T C N G** - 3', where **N** stands for the four nucleotides, **R** = A and G, **Y** = T and C, **H** = T, C, and A, is derived from the first 8 amino acids of the protein (AKEIKFSD); the second one 5' - **C R T T N C K N C C N C K N G G N C C C A T** - 3', where **K** = G and T, corresponds to the complementary codons specifying the amino acid from position 29 to position 36 (MGPRGRNV, Evans et al. 1992, Inf. Immun., 60:2125-2127). The expected size for the PCR product was 108 base pairs (bp). The amplification reaction was performed under low stringency conditions as described in the Materials and Methods section, and led to the synthesis of six fragments with sizes ranging from 400 bp to 100 bp. The three smallest fragments were electroeluted from an acrylamide gel and purified. Direct sequencing of the PCR products permitted the identification of a DNA fragment encoding an amino acid sequence corresponding to the published sequence. This fragment was, therefore, labeled and used as probe in colony hybridization to identify recombinant cosmids exhibiting homology to a 5' segment of the *H. pylori* GroEL-like encoding gene; this gene was further designated *hspB*. The gene bank consists of 400 independent kanamycin-resistant *E. coli* transductants harboring recombinant cosmids. Of those, one single clone hybridized with the probe and harbored a recombinant plasmid designated pILL684, 46 kb in size. The low frequency observed when detecting the *hspB* gene (1 of 400) was unusual when compared with that of several cloned genes, which were consistently detected in five to seven recombinant cosmids. In order to identify the *hsp*B gene, fragments with sizes of 3 to 4 kb were generated by partial restriction of the pILL684 cosmid DNA with endonuclease *Sau*3A, purified, and ligated into the *Bgl*II site of plasmid vector pILL570. Of 100 subclones, 7 were positive clones, and one was further

studied (pILL689) (Table 5); it contains a 3.15 kb insert, flanked by two *Bgl*II restriction sites, that was mapped in detail (Fig. 5). Using the PCR ^{32}P labeled probe, the 5' end of the *hspB* gene was found to map to the 632 bp *Hind*III-*Sph*I central restriction fragment of pILL689, indicating that one could expect the presence of the entire *HspB* gene in the pILL689 recombinant plasmid.

2. DNA sequence and deduced amino acid sequence of the *H. pylori HspA-B* gene cluster:

The 2300 bp of pILL689 depicted in Fig. 5 were sequenced by cloning into M13mp18 and M13mp19, the asymmetric restriction fragments *Bgl*II-*Sph*I, *Sph*I-*Hind*III, *Hind*III-*Bgl*II; each cloned fragment was independently sequenced on both strands, 16 oligonucleotide primers were synthesized to confirm the reading and/or to generate sequences overlapping the independently sequenced fragments; these were used as primers in double-stranded DNA sequencing analyses.

The analysis of the sequence revealed two distinct genetic elements. First the presence of two open reading frames (ORFs), depicted in Figure 5, transcribed in the same direction, that were designated *hspA* and *hspB*. The nucleotide sequence and the deduced amino acid sequence of the two ORFs are presented in Fig. 6. The first codon of *hspA* begins 323 bp upstream of the leftward *Hind*III site of pILL689 (Fig. 5) and is preceded by a Shine-Dalgarno ribosome-binding site (RBS) (**GGAGAA**). The *hspA* ORF codes for a polypeptide of 118 amino acids. The initiation codon for the *hspB* ORF begins 25 nucleotides downstream the *hspA* stop codon; it is preceded by a RBS site (**AAGGA**). *hspB* ORF encodes a polypeptide of 545 amino acids and is terminated by a TAA codon followed by a palindromic sequence resembling a rho-independent transcription terminator (free energy, Δ = -19.8 kcal/mol) (Fig. 6). The N-terminal amino acid sequence of the deduced protein HspB was identical to the N-terminal sequence of the purified *H. pylori* heat shock protein previously

published with the exception of the N-terminal methionine, which is absent from the purified protein and might be post-translationally removed, resulting in a mature protein of 544 amino acids.

The deduced amino acid sequences of *H. pylori* HspA and HspB were compared to several amino acid sequences of Hsps of the GroES and GroEL class (Fig. 7). HspB exhibited high homology at the amino acid level with the *Legionella pneumophila* HtpB protein (82.9% of similarities), with the *Escherichia coli* GroEL protein (81.0% of similarities), with the *Chlamydia psittaci* or *C. trachomatis* HypB protein (79.4% of similarities), with *Clostridium perfringens* Hsp60 protein (80.7% of similarities), and to a lesser extent to the GroEL-like proteins of *Mycobacterium*. However, like almost all the GroEL homologs, *H. pylori* HspB demonstrated the conserved carboxyl-terminus glycine-methionine motif (MGGMGGMGGMGGMM), which was recently shown to be dispensable in the *E. coli* GroEL chaperonin. The degree of homology at the amino acid level between the *H. pylori* HspA protein and the other GroES-like proteins is shown in Fig. 7. The alignment shown features a striking motif at the carboxyl terminus of the *H. pylori* HspA protein that other bacterial GroES-homologs lack. This unique highly charged motif consists of 27 additional amino acids capable of forming a loop between two double cysteine residues; of the 27 amino acids, 8 are histidine residues highly reminiscent of a metal binding domain.

The second genetic element revealed by the sequence analysis, was the presence of an insertion sequence (IS5) 84 bp upstream of the *hspA* gene. The nucleotide sequence of this element matched perfectly that previously described for IS5 in *E. coli*, with the presence of a 16 nucleotide sequence (CTTGTTCGCACCTTCC) that corresponds to one of the two inverted repeats, which flank the IS5 element. Because of the perfect match at the DNA level, we suspected that the IS5 was not initially present in the *H. pylori* chromosome, but

had rather inserted upstream of the *HspA-HspB* gene cluster during the cloning process, a hypothesis that needed to be confirmed by further analyses.

3. Identification of the upstream sequence of theHspA-B gene cluster in *H. pylori* chromosome:

The presence of the IS5 was examined by gene amplification using two oligonucleotides, one being internal to the IS5 element and the other one downstream of the IS5 element to target a putative sequence i) in the chromosome of *H. pylori* strain 85P, ii) in the initial cosmid pILL684 (Table 5), and iii) in the 100 subclones resulting from the *Sau*3A partial restriction of the pILL684 recombinant cosmid. IS5 was absent from the chromosome of *H. pylori*, and was present in the very first subcultures of the *E. coli* strain harboring cosmid pILL684. Among the 100 pILL684 subclone derivatives that appeared to contain all or part of the IS5 sequence, we then looked for a subclone harboring the left end side of the IS5 plus the original upstream sequence of the *HspA-HspB* gene cluster. This screening was made by restriction analysis of the different *Sau*3A partial generated subclones. The restriction map of one (pILL694) of the plasmids fulfilling these criteria is shown in Suerbaum et al., 1996, Molec. Microbiology. The left end side of the IS5 nucleotide sequence was determined; the presence of a 4-bp duplication CTAA on both sides of the 16-bp inverted repeats of the IS5 element allowed us to confirm the recent acquisition of the IS5 element by transposition. A 245-nucleotide sequence was then determined that mapped immediately upstream of the IS5 element. This sequence consists of a non-coding region in which the presence of a putative consensus heat shock promoter sequence was detected; it shows a perfectly conserved -35 region (**TAACTCGCTTGAA**) and a less consentaneous -10 region (CTCAATTA). Two oligonucleotides were synthesized, which mapped to sequences located on both sides of the IS5 element present in the recombinant cosmid; these two oligonucleotides should lead to the amplification of a 350bp fragment when the

polypeptides visualized on the SDS gel was in good agreement with the copy number of the respective vectors, the intensity of the two polypeptidic bands suggested a polycistronic transcription of the two genes.

5. Attempts to understand the role of the HspAand HspB proteins:

Two disruptions of genes were achieved in *E. coli* by inserting the Km cassette previously described within the *hspA* or the *hspB* gene of plasmids pILL686 and pILL691. This was done in order to return the disrupted genes in *H. pylori* by electroporation, and to select for allelic replacement. The pILL696 resulting plasmid encoded a truncated form of the HspA protein, corresponding to the deletion of the C-terminal end amino acid sequence, in that plasmid the Km cassette was inserted in such way that the promoter of the Km gene could serve as promoter for the *HspB* downstream gene. The pILL687 and pILL688 plasmids (Table 5) resulted from the insertion of the Km cassette in either orientation within the *hspB* gene. None of these constructs led to the isolation of kanamycin transformants of *H. pylori* strain N6, when purified pILL687, pILL688, pILL696 plasmids (Table 5) were used in electroporation experiments, whereas the pSUS10 plasmid used as positive control always did. These results suggest the *H. pylori* HspA and HspB protein are essential proteins for the survival of *H. pylori*.

Because of i) the constant description in the literature of a close association of the HspB protein with the urease subunits; ii) the unique structure of the HspA protein with the C-terminal sequence reminiscent of a nickel binding domain, and iii) of the absence of viable *HspA* and/or *HspB* mutants of *H. pylori*, we attempted to demonstrate a role of the *H. pylori* Hsp proteins in relation with the *H. pylori* urease by functional complementation experiments in *E. coli*. Plasmids pILL763 or pILL753 (both pILL570 derivatives, Table 5) encoding the urease gene cluster were introduced with the compatible pILL692 plasmid

(pACYC177 derivative) that constitutively expresses the HspA and HspB polypeptides as visualized in minicells. In both complementations, the expression of the HspA and HspB proteins in the same *E. coli* cell allows to observe a three-fold increase in the urease activity following induction of the urease genes on minimum medium supplemented with 10 mM L^{-1} arginine as limiting nitrogen source.

Table 5: Vectors and hybrid plasmids used in this study.

Plasmid	Vector	Size(kb)	Characteristics(a)	Origin or Reference
	pILL575	10	Mob, Cos, Km	-
	pILL570	5.3	Mob, Sp	-
	pACYC177	3.9	Ap,Km	-
pILL600	pBR322	5.7	Ap, Km, source of Km-cassette	-
pILL684	pILL575	46	Mob, Km, cosmid containing *H. pylori hspA-B*	*Sau*3A partial digest of *H. pylori* 85P DNA
pILL685	pILL570	9.29	Mob, Sp, plasmid containing *H. pylori hspB*	*Sau*3A partial digest of pILL684
pILL686	pUC19*c	4.5	Ap, plasmid containing *H. pylori hspB*	1.9-kb *Bg*III-*Cla*I pILL685 cloned into pUC19*
pILL687	pUC19*(c)	5.9	Ap, Km, *H. pylori hspB* Ω Km-orientation A(b)	1.4-kb *Sma*I-*Sma*I pILL600 cloned into pILL686
pILL688	pUC19*(c)	5.9	Ap, Km, *H. pylori hspB* Ω Km-orientation B(b)	1.4-kb *Sma*I-*Sma*I pILL600 cloned into pILL686
pILL689	pILL570	8.45	Mob, Sp, plasmid containing *H. pylori hsp A-B*	*Sau*3A partial digest of pILL684
pILL691	pUC19**(c)	3.9	Ap, plasmid containing *H. pylori hspA* 1.3-kb	*Sph*I-*Sph*I pILL689 cloned into pUC19**
pILL692	pACYC177	7.05	Ap, Km, plasmid containing *H. pylori hspA-B*	3.15-kb*Bg*III pILL689 cloned into pACYC177
pILL694	pILL570	8.7	Sp, plasmid containing left end of IS5	*Sau*3A partial digest of pILL684
pILL696	pUC19**(c)	5.3	Ap, Km, *H. pylori hspA* Ω Km-orientation A (b)	1.4-kb *Sma*I-*Sma*I pILL600 cloned into pILL691
pSUS10	pIC20R2	7.7	Ap, Km, *H. pylori flaA* Ω Km	-
pILL753	pILL570	16.5	Sp, plasmid containing *ureA,B,C,D,E,F,G,H,I*	-
pILL763	pILL570	14.75	Sp, plasmid containing *ureA,B,E,F,G,H,I*-	-

(a) Mob, conjugative plasmid due to the presence of OriT; Ap, Km and Sp, resistance to ampicillin, kanamycin, and spectinomycin, respectively; Cos, presence of lambda cos site.
(b) Orientation A indicates that the Kanamycin promoter initiates transcription in the same orientation as that of the of the gene where the cassette has been inserted; orientation B, the opposite.
(c) pUC19* and pUC19**: derivatives from pUC19 vector in which the SphI and HindIII site, respectively, have been end-filled by using the Klenow polymerase and self religated.

IV. Expression, Purification And Immunogenic Properties Of *H. Pylori* HspA AND HspB:

A. Experimental Procedure For Part IV:

Expression and purification of recombinant fusion proteins:

The MalE-HspB fusion proteins were expressed following the cloning of the two genes within the pMAL-c2 vector as described in the "Results" section using the following primers:

oligo #1 ccggagaattcAAGTTTCAACCATTAGGAGAAAGGGTC
oligo #2 acgttctgcagTTTAGTGTTTTTTGTGATCATGACAGC
oligo #3 ccggagaattcGCAAAAGAAATCAAATTTTCAGATAGC
oligo #4 acgttctgcagATGATACCAAAAAGCAAGGGGGCTTAC

Two liters of Luria medium containing glucose (30%) and ampicillin (100 μg/ml) were inoculated with 20 ml of an overnight culture of strain MC1061 containing the fusion plasmid and incubated with shaking at 37°C. When the OD600 of the culture reached 0.5, IPTG (at a final concentration of 10 mM) was added, and the cells were incubated for a further 4 hours. Cells were harvested by centrifugation (5000 rpm for 30 min at 4°C), resuspended in 100 ml of column buffer consisting of 10 mM Tris-HCl, 200 mM NaCl, 1 mM EDTA supplemented with protease inhibitors [(Leupeptin (2 μM) - Pepstatin (2 μm) - PMSF (1mM) - Aprotinin (1:1000 dilution)], and passed through a French press. After centrifugation (10,000 rpm for 20 min at 4°C), the supernatant were recovered and diluted (2-fold) with column buffer. The lysate was filtered through a 0.2 μm nitrocellulose filter prior to loading onto a pre-equilibrated amylose resin (22 x 2.5 cm). The fusion proteins were eluted with a 10mM maltose solution prepared in column buffer, and the fractions containing the fusion proteins were pooled, dialyzed against distilled water, and lyophilized. Fusion proteins were resuspended in distilled

water at a final concentration of 2 mg of lyophilized material/ml, and stored at -20°C. Concentration and purity of the preparations were controlled by the Bradford protein assay (Sigma Chemicals) and SDS-PAGE analyses.

2. Nickel binding properties of recombinant proteins:

E. coli MC1061 cells, containing either the pMAL-c2 vector or derivative recombinant plasmids, were grown in 100 ml-Luria broth in the presence of carbenicillin (100 μg/ml). The expression of the genes was induced with IPTG for four hours. The cells were centrifuged and the pellet was resuspended in 2 ml of Buffer A (6M guanidine hydrochloride, 0.1 M NaH_2PO_4, 0.01 Tris, pH 8.0). After gentle stirring for one hour at room temperature, the suspensions were centrifuged at 10,000 g for 15 min at 4°C. A 1.6 ml aliquot of Nickel-Nitrilo-Tri-Acetic resin (Nickel-NTA, QIA Express), previously equilibrated in Buffer A, was added to the supernatant and this mixture was stirred at room temperature for one hour prior to loading onto a column. The column was washed with 20 ml buffer A, then 30 ml buffer B (8M urea, 0.1M Na-phosphate, 0.01M Tris-HCl, pH8.0). The proteins were eluted successively with the same buffer as buffer B adjusted to pH 6.3 (Buffer C), pH 5.9 (Buffer D) and pH 4.5 (Buffer E) and Buffer F (6M guanidine hydrochloride, 0.2 M acetic acid). Fifty μl of each fraction were mixed with 50 μl of SDS buffer and loaded on SDS gels.

3. Human sera:

Serum samples were obtained from 40 individuals, 28 were *H. pylori*-infected patients as confirmed by a positive culture for *H. pylori* and histological examination of the biopsy, and 12 were uninfected patients. The sera were kindly provided by R. J. Adamek (University of Bochum, Germany).

4. Immunoblotting:

Upon completion of SDS-PAGE runs in a Mini-PROTEAN II electrophoresis cell, proteins were transferred to nitrocellulose paper in a Mini Trans-Blot transfer cell (Bio-Rad) set at 100 V for 1 h (with cooling).

Immunostaining was performed as previously described (Ferrero et al., 1992), except that the ECL Western blotting detection system (Amersham) was used to visualize reaction products. Human sera and the rabbit antiserum, raised against a whole-cell extract of *H. pylori* strain 85P, were diluted 1:1000 and 1:5000, respectively, in 1% (w/v) casein prepared in phosphate-buffered saline (PBS, pH7.4).

5. Serological methods [enzyme-linked immunosorbent assay, (ELISA)]:

The following quantities of antigens were absorbed onto 96-well plates (Falcon 3072): 2.5 μg of protein MalE, 5 μg of MalE-HspA, or 2.5 of μg of MalE-HspB. The plates were left overnight at 4°C, then washed 3 times with ELISA wash solution (EWS) [1% PBS containing 0.05% (v/v) Tween 20]. Saturation was achieved by incubating the plates for 90 min at 37°C in EWS supplemented with 1% milk powder. Wells were again washed 3 times with EWS and then gently agitated for 90 min at 37°C in the presence of human sera (diluted 1:500 in EWS with 0.5% milk powder), under agitation. Bound immunoglobulins were detected by incubation for 90 min at 37°C with biotinylated secondary antibody (goat anti-human IgG, IgA or IgM diluted [1:1000] in EWS supplemented with 0.5% milk powder) in combination with streptavidin-peroxidase (1:500) (Kirkegaard and Perry Lab.). Bound peroxidase was detected by reaction with the citrate substrate and hydrogen peroxide. Plates were incubated in the dark, at room temperature, and the optical density at 492 nm was read at intervals of 5, 15 and 30 min in an ELISA plate reader. After 30 min, the reaction was stopped by the addition of hydrochloric acid to a final concentration of 0.5M.

B. Results Of Part IV Experiments:

1. Construction of recombinant plasmids producing inducible MalE-HspA, and HspB fusion proteins:

The oligonucleotides #1 and #2 (*HspA*) and #3 and #4 (*HspB*) were used to amplify by PCR the entire *HspA* and the *HspB* genes, respectively. The PCR products were electroeluted, purified and restricted with *Eco*RI and *Pst*I. The restricted fragments (360 bp and 1600 bp in size, respectively) were then ligated into the *Eco*RI-*Pst*I restricted pMAL-c2 vector to generate plasmids designated pILL933 and pILL934, respectively. Following induction with IPTG, and purification of the soluble protein on amylose columns, fusion proteins of the expected size (55 kDa for pILL933 [Figure 17], and 100 kDa for pILL9334) were visualized on SDS-PAGE gels. Each of these corresponded to the fusion of the MalE protein (42.7 kDa) with the second amino acid of each of the Hsp polypeptides. The yield of the expression of the fusion proteins was 100 mg for MalE-HspA and 20 mg for MalE-HspB when prepared from 2 liters of broth culture.

2. Study of the antigenicity of the HspA and HspB fusion proteins, and of the immunogenicity of HspA and HspB in patients infected with *H. pylori*:

In order to determine whether the fusion proteins were still antigenic, each was analyzed by Western blot with rabbit antiserum raised against the MalE protein and a whole-cell extract of *H. pylori* strain 85P. Both fusion proteins were immunoreactive with antibody to MalE (not shown) and with the anti-*H. pylori* antiserum. The anti-*H. pylori* antiserum did not recognize the purified MalE protein (Fig. 18). These results demonstrated that the fusion proteins retained their antigenic properties; in addition, whereas the HspB protein was known to be immunogenic, this is the first demonstration that HspA *per se* is immunogenic in rabbits.

In the same way, in order to determine whether the HspA and HspB polypeptides were immunogenic in humans, the humoral immune response against HspA and/or HspB in patients infected with *H. pylori* was analyzed and compared to that of uninfected persons using Western immunoblotting assays and enzyme-linked immunosorbent assays (ELISA). None of the 12 sera of the *H. pylori*-negative persons gave a positive immunoblot signal with MalE, MalE-HspA, or MalE-HspB proteins (Fig. 18). In contrast, of 28 sera from *H. pylori*-positive patients, 12 (42.8%) reacted with the HspA protein whilst 20 (71.4%) recognized the HspB protein. All of the sera that recognized HspA also reacted with the HspB protein. No association was observed between the immune response and the clinical presentation of the *H. pylori* infection although such a conclusion might be premature because of the small number of strains analyzed.

3. Nickel binding properties of the fused MalE-HspA protein:

MBP-HspA recombinant protein expressed following induction with IPTG was purified from a whole cell extract by one step purification on nickel affinity column whereas the MBP alone, nor MBP-HspB exhibited this property. Figure 18 illustrates the one step purification of the MBP-HspA protein that was eluted as a monomer at pH 6.3, and as a monomer at pH 4.5. The unique band seen in panel 7 and the two bands seen in panel 5 were both specifically recognized with anti-HspA rabbit sera. This suggested that the nickel binding property of the fused MBP-HspA protein might be attributed to the C-terminal sequence of HspA, which is rich in histidine and cysteine residues.

V. Immunication with *Helicobacter Pylori* GroES Homolog and Urease Subunit Proteins Affords Total Protection Against Mucosal Infection.

Helicobacter pylori is an etiological agent of chronic gastritis and peptic ulceration. Whilst a significant proportion of the population is infected by *H. pylori* bacteria, infected individuals do not always experience symptoms. Recent investigations have established a causal relationship between *H. pylori* and carcinogenesis, which has led to WHO/IARC to classify *H. pylori* as a "definite human carcinogen." Long-term *H. pylori* colonization of the gastric mucosa is involved in the formation of gastric atrophy, which is a known precursor of gastric cancer. It is, therefore, feasible to suggest that prophylaxis against *H. pylori* infection, as well as reducing the incidence of peptic ulcer disease, may also reduce the cases of gastric neoplasia. We believe that for such a strategy to succeed it will be necessary to target properties that are shared by all isolates of *H. pylori*.

Urease activity is a property common to all *H. pylori* isolates and is essential for colonization of the gastric mucosa. *H. pylori* urease is composed of two subunits (UreA and UreB), which from a high molecular weight complex with nickel ions. These subunits are immunodominant antigens and are highly conserved between the different gastric *Helicobacter* species, including *Helicobacter felis*.

In common with other organisms, *H. pylori* bacteria express heat-shock proteins that share homologies with the GroES and GroEL class of proteins from *Escherichia coli*. We have assessed the heat-shock proteins of *H. pylori* as potential protective antigens in a murine model of gastric *Helicobacter* infection. Orogastric immunization of mice with recombinant *H. pylori* GroES- and GroEL-like proteins protected 80% (n=20) and 70% (n=10) of animals, respectively, from a challenge dose of 10^4 *Helicobacter* bacteria (versus control mice: P=0.0042 and P=0.0904, respectively). All mice (n=19) that were immunized with a dual

antigen preparation, consisting of *H. pylori* GroES-like protein and the B subunit of *H. pylori* urease, were protected against infection. This represented an equivalent level of protection as that provided by a sonicated *Helicobacter* extract (P=0.955). Antibodies directed against the recombinant *H. pylori* antigens were predominantly of the IgG_1 class, suggesting a type 2 T-helper cell (Th-2) response was involved in protection.

Finally, GroES-like and urease subunit B proteins have been identified as potential components of a future *H. pylori* subunit vaccine. Presented below are data showing that the co-administration of an immunization composition of two defined antigens, *H. pylori* UreB and HspA, was able to confer a level of protection equivalent to that induced by a whole-cell preparation.

Experimental Procedures for Part V

A. Materials and Methods

1. Bacterial Strains, Media and Growth:

H. pylori (85P) was a clinical isolate. Labigne et al., J. Bacteriol, 173, 1920-1931 (1991). *H. felis* (ATCC 49179) was originally isolated from cat gastric mucosa. Lee (1988). *Helicobacters* were grown on a blood agar medium, containing an antibiotic mixture, and incubated under microaerobic conditions at 37°C. Ferrero (1993). *Escherichia coli* MC1061 cells were grown routinely at 37°C, in solid or liquid Luria medium.

2. Production of Recombinant *H. pylori* antigens:

The genes encoding *H. pylori* urease subunit B and HSP polypeptides (*UreB*, *HspA* and *HspB*, respectively) were each cloned into the expression vector pMAL-C2 (New England Biolabs Inc.), as previously described. Ferrero (1994) Infect. Immunol. 62, 4981-4989. Recombinant *H. pylori* proteins were expressed as MalE fusions. *E. coli* MC1061 cells harboring the recombinant

plasmids were induced with isopropyl-β-D-thiogalactopyranoside (IPTG), and the fusion proteins purified from culture supernatants by affinity and anion exchange chromatography. The purity of recombinant protein preparations was analyzed by SDS-PAGE and by immunoblotting.

3. SDS-PAGE and Immunoblotting Techniques:

Solubilized protein preparations were analyzed on slab gels, comprising a 4.5% acrylamide stacking gel and a 12.5% resolving gel, according to the procedure of Laemmli. Proteins were transferred to nitrocellulose membranes in a Mini Trans-Blot transfer cell (Bio-Rad). Immunoreactants were detected by chemiluminescence (ECL System, Amersham). Ferrero (1994).

Protein concentrations were determined by the Bradford assay (Sigma Chemical Co., St. Louis, Mo.).

4. Animal Experimentation:

Four to 6 wk-old Swiss specific-pathogen-free mice (Centre d'Elevage R. Janvier, Le-Genest-St-Isle, France) were fed a commercial pellet diet with water *ad libitum*. These mice were previously shown to be free of the murine *Helicobacter sp*, *Helicobacter muridarum* (Ferrero 1994). Aliquots (0.1 ml) containing 10^4 *H. felis* bacteria prepared from a low-subculture stock suspension of *H. felis* were administered orogastrically to mice, as previously described (Ferrero 1994). Antigen extracts (50 µg protein) containing 5 µg cholera toxin (Sigma) were prepared in 0.1 M sodium bicarbonate, prior to delivery to mice. Following sacrifice, stomachs were removed and sera collected.

H. felis colonization was assessed using the biopsy urease test and histological techniques. Portions of gastric antrum and body were placed on the surfaces of individual agar plates (1 cm by 1 cm) containing a modified Christensen's medium, to which had been added a *Helicobacter*-selective antibiotic mixture. The plates were observed for up to 48 h. The remaining two-thirds of each stomach were dissected into longitudinal segments

(approximate width 2 mm), which were processed for histopathology (Ferrero 1994).

So as to eliminate observer bias, Giemsa-stained sections were coded prior to histological assessment. For each stomach, all the available tissue (representing up to 2/3 of the stomach) was scrutinized. Protection from *H. felis* colonization w[illegible]efined as the absence of *H. felis* bacteria from the totality of sections repres[illegible]ch stomach. The severity of gastritis was assessed on the basis of both t[illegible]ree of mononuclear cell infiltration as well as the distribution of the cel[illegible] Thus, gastritis was scored according to the following scale: 0, no [illegible]cant infiltration; 1, infiltration of low numbers of lymphocytes, limited to the muscularis mucosa and the submucosa; 2, infiltration of moderate numbers of lymphocytes in the submucosa, with variable numbers extending into the mucosa; and 3, infiltration of large numbers of lymphocytes in the mucosa, leading to the formation of several aggregates or even nodular structures.

5. ELISA:

Seric IgG antibodies in immunized mice were detected by ELISA. Sauerbaum et al., Molec. Microbiol. 14, 959-974 (1994). Briefly, 96-well plates (Nunc Maxisorb) were coated with a sonicated extract of *H. pylori* (25 μg protein per well). Bound IgG were detected with biotinylated goat anti-mouse antibodies (Amersham) and streptavidin-peroxidase conjugate. Immune complexes were detected by reaction with a solution containing o-phenylenediamine dihydrochloride (Sigma) and hydrogen peroxide. Optical density readings were read at 492 nm in an ELISA plate reader (Titertek).

6. Statistics:

Data were analyzed by X^2 and Xc^2 (with Yate's correction) tests as appropriate (Campbell et al., Medical Statistics. A Commonsense Approach, 2nd

Ed., John Wiley, Chichester (1993)), using the Statview 512+ computer software package (BrainPower, Inc., Calabasas, CA).

B. Results of Part V Experiments

1. Determination of the Minimum Infectious Dose for *H. felis* in the Mouse:

The *H. felis*-infected mouse has become the model of choice for trials aimed at identifying antigens that may serve in a future *H. pylori* vaccine. Thus far, the size of the *H. felis* inoculum used to challenge immunized animals has not been reconciled with the low *H. pylori* bacterial load that a vaccinated, non-infected individual would be expected to encounter when exposed to *H. pylori*-infected persons. To this end, we have determined the minimum infectious dose required to colonize Swiss mice with *H. felis* (under the conditions in our laboratory). Groups of five mice were thus colonized with inocula prepared from virulent *H. felis* bacteria, which varied from 10^1 to 10^5 bacteria. The results are shown in Table 6.

Table 6. Determination of the minimum infectious dose for *H. felis* in mice.

Identification of *H. felis* infection in mice at 2 wk post-inoculation		
Inoculum dose* (no. of bacteria)	Urease activity§ (no.)	Culture¶ (no.)
10^1	0/5	0/5
10^2	4/5	3/5
10^3	5/5	4/5
10^4	5/5	3/5
10^5	4/5	4/5

*To determine cell density, various dilutions of a stock *H. felis* culture (which contained predominantly helical-shaped forms) were prepared. Viable *H. felis* bacteria were then enumerated under phase contrast microscopy (magnification factor, 400 x), using a Malassez chamber. Mice were inoculated orogastrically with 0.1 ml of the appropriate inoculum containing virulent *H. felis* bacteria.

§Urease activity was detected in murine gastric biopsies (see *Materials and Methods*).

¶*H. felis* bacteria were isolated from gastric tissue biopsies after incubation on blood agar plates under microaerobic conditions for 5-7 days, at 37°C.

Whilst an inoculum containing *c.* 10^1 bacteria was found to be insufficient to colonize mice, gastric infection in mice was achieved with inocula containing at least 10^2 bacteria (the minimum infectious dose). A challenge inoculum equivalent to 100 times the minimum infectious dose (*i.e.* 10^4 bacteria) was subsequently chosen for all immunoprotection studies.

2. Protection Against H. *felis* Infection in Mice by Immunization with Recombinant HSPs from *H. pylori*.

To demonstrate the presence of HSP homologs in *H. felis*, whole-cell extracts of the organism were immunoblotted and then reacted with hyperimmune rabbit antisera raised against *H. pylori* MalE-HspA and MalE-HspB fusions. Cross-reactive antigens were detected in the *H. felis* extract: the denatured antigens had approximate molecular weights of 15 kDa and 58 kDa, respectively, which corresponded to those of the *H. pylori* HSPs (Figs. 20A, B). Interestingly, it appeared that the HspA homologs of both *H. pylori* and *H. felis* exist in dimeric forms and these multimeric forms appeared to be resistant to the denaturing effects of SDS.

Recombinant *H. pylori* HSP antigens were assessed for their potential to induce protective mucosal responses in the *H. felis* mouse model. Mice were immunized once per wk (wks 0 to 3) with 50 mg antigen (or 1 mg *H. felis* whole-cell sonicate) and 5 mg cholera toxin. At wk 5, the mice were challenged with an inoculum containing c. 10^4 *H. felis* bacteria. At wk 7, the mice were sacrificed. The results are reported in Table 7.

Table 7. Immunization of mice against *H. felis* infection using *H. pylori* antigens

	infectious stat[illegible]		Grade of gastritis[g]	
Antigens	Infected (no.)	Not infected[f]	Infected	Not infected[f]
MalE (M)	14/20	30%	2.57 ± 0.65 (14)	1.0 ± 0 (6)
sonicate[a]	1/17	94	3 (1)	1.31 ± 0.79 (16)
M-HspA[b]	4/20	80	3 (4)	1.19 ± 0.83 (16)
M-HspB[c]	3/10	70	3 (3)	1.0 ± 0.82 (7)
M-UreB[d]	3/21	86	2.3 (3)	1.17 ± 0.38 (18)
M-HspA/UreB[e]	0/19	100	(h)	1.53 ± 0.70 (19)
			Σ 2.68 ± 0.56 (25)[h]	1.28 ± 0.71 (82)i

[a]*P*=0.0003; [b]*P*=0.0042; [c]*P*=0.0904; [d]*P*=0.001; [e]*P*=0.0001 compared with the MalE group of animals.

[f]Mice were considered "not infected" when the biopsy urease test was negative, and no *H. felis* bacteria were detected in coded histological sections (see *Materials and Methods*).

[g]Gastitis was scored from 0 to 3 (see *Materials and Methods*). Mean scores ± S.D. are presented. Numbers in paragraphs refer to the numbers of animals per group.

[g]Gastitis was scored from 0 to 3 (see *Materials and Methods*). Mean scores ± S.D. are presented. Numbers in paragraphs refer to the numbers of animals per group.

[h]No mice from this group were infected.

[i]Comparison of score frequencies between immunized animals that became infected and those that were protected (P=0.0001).

[h]Comparison of individual scores between immunized animals that became infected and those that were protected (P=0.0001).

Immunization with HspA- or HspB-MalE fusions protected 80% and 70%, respectively, of mice against *H. felis* infection (Table 7). In comparison, 30% of MalE-immunized control mice did not become infected when challenged with the *H. felis* inoculum (P=0.0042 and P=0.0904, respectively).

Co-administration of recombinant *H. pylori* UreB and HspA antigens to mice resulted in 100% protection, which compared with a protection rate of 86% in those animals that had received the UreB antigen alone (Table 7). The level of protection afforded by the co-administration of MalE-UreB and MalE-HspA was equivalent to that obtained in the group of *H. felis* sonicate-immunized animals (P=0.955; Table 7).

3. Serological Responses Following Immunization with Recombinant HSPs and Urease Polypeptides:

Measurement of *H. pylori*-specific IgG antibodies in the serum of immunized mice demonstrated that virtually all of the animals developed strong humoral responses to the administered *H. pylori* urease and heat-shock antigens. As would be predicted of a mucosal immune response, serum antibodies directed against these antigens appeared to be primarily of the IgG_1

idiotype (Fig. 19). This finding was indicative of a predominantly type 2 T-helper cell (Th-2) response. Consistent with this, serum levels of *H. pylori*-specific IgG_{2a} antibodies, which are normally associated with Th-1 type responses, were relatively low and varied depending upon the antigen administered: HspA appeared to induce particularly weak IgG_{2a} serum responses (Fig. 19). These differences were considered to be specific to the *H. pylori* antigenic components of the recombinant proteins, since approximately equivalent levels of IgG_1 and IgG_{2a} antibody idiotypes were detected when MalE-specific antibodies were measured (unpublished data). No qualitative nor quantitative differences could be found between IgG serum responses and the infectious status of the mice at sacrifice.

4. Cellular Responses Induced in Mice following Immunization:

Histological assessment of gastric mucosa tissue from the immunized mice revealed low levels of mononuclear cells (mean inflammation score: 1.28 ± 0.71) for those mice which were protected from an *H. felis* infection (Table 7). In contrast, those immunized animals that became infected tended to have a significantly more severe form of lymphocytic gastritis in which lymphoid follicular structures were often observed (mean score: 2.68 ± 0.56; P=0.0001). Large numbers of mononuclear cells were observed in the gastric tissue of *H. felis*-colonized mice from the MalE-immunized group.

In this study, we tested an antigenic preparation consisting of two recombinant proteins, *H. pylori* UreB and HspA, and showed that, under identical experimental conditions, it was as effective as a whole-cell extract of *H. felis* in protecting against *H. felis* infection in mice. We observed in both this study, and in an independent one in which immunized mice were not challenged with *H. felis* (unpublished data), that the administration of *H. pylori* Hsp antigens did not appear to be associated with an unduly severe pathology.

The evidence to date suggests that a mild gastric inflammation may be a necessary prerequisite for a successful orogastric immunization. Michetti et al., Gastroenterology 107, 1002-1011 (1994); Ferrero (1994). Activation of a Th-2 immune response is normally associated with the migration of both IgA-secreting B lymphocytes and T_H lymphocytes to effector tissue sites. Staats et al., Curr. Opin. Immunol. 6, 572-583 (1994). It is, therefore, perhaps not surprising that orogastric immunization of mice results in a mild degree of lymphocytic gastritis. Administration of cholera toxin may contribute to this inflammation: *in vitro* experiments showed that cholera toxin alone increased the proliferation of murine B and T lymphocytes. Elson, Infect. Immun. 60, 2874-2879 (1992). It is also likely that the antigenic load provided by the *H. felis* bacterial challenge exacerbates the inflammation: immunized mice that became infected with *H. felis* displayed a higher degree of gastritis than those immunized animals that were protected against *H. felis* infection. However, as this difference was also observed amongst the MalE-immunized group of mice, it is unlikely that cross-reactivity between the recombinant *H. pylori* antigens and the *H. felis* bacteria accounted for the severe pathology seen in those immunized mice that were not protected. Eaton and Krakowka also observed that immunized piglets, which were not protected against *H. pylori* infection, developed severe gastritis. Eaton et al., Gastroenterology 103, 1580-1586 (1992).

H. pylori HspA is particularly appealing as a vaccine component because, in contrast with HspB, it possesses a unique domain at its C-terminus, which is absent from other known heat-shock homologs, including those of eucaryotic organisms. The C-terminus of *H. pylori* HspA consists of a series of 26 amino acids (out of a total of 118 amino acids), and undoubtedly confers a unique conformational structure to this polypeptide. The capacity of *H. pylori* HspA to bind to nickel ions should facilitate the large-scale purification of this polypeptide by metal affinity chromatography.

Evidence from the immunoprotection studies and immunoblot analyses suggest that *H. felis* produces a GroES homolog. Whether this protein also contains the C-terminal nickel-binding domain is currently a subject of investigation in our laboratory. It is noteworthy that these *Helicobacter* GroES homologs seem to exist as dimeric forms, a feature that has also been described for other known nickel-binding proteins, such as the UreE proteins from *Proteus mirabilis*, Sriwanthana et al., J. Bacteriol, 176, 6836-6841 (1994), and *Klebsiella aerogenes*, Lee et al., Protein Sci. 2, 1042-1052 (1993).

Thus, the immunization composition of this invention preferably contains *H. pylori* UreB and HspA as immunogens. The UreB and HspA can be isolated from *H. pylori* lysates or sonicates, but are preferably free of other *H. pylori* antigens, including multimeric urease. Thus, in one embodiment of the invention the UreB and HspA are substantially free of UreA. It is particularly preferred that the UreB and the HspA be prepared by recombinant techniques. The resulting recombinant antigens are substantially free of multimeric urease and other *H. pylori* antigens.

The immunization composition of the invention can also include an adjuvant in an amount sufficient to enhance the magnitude or duration of the immune response in the host, or to enhance the qualitative response in the subject, such as by stimulating antibodies of different immunoglobulin classes than those stimulated by the immunogen. The adjuvant should efficiently elicit cell-mediated or humoral immune responses to antigens without systemic or localized irritation of the host system. Preferably, the adjuvant has low pyrogenicity.

Well known adjuvant formulations for human or veterinary applications can be employed. Such adjuvants can be based on emulsions, with or without mycobacteria, or adjuvants based on adsorption of antigens to aluminum salts, especially aluminum hydroxide or aluminum phosphate. Among these adjuvants

are oil adjuvants based on mineral, animal, and vegeTable oils. Oil based adjuvants are useful for increasing humoral responses of animals to vaccine antigens, and certain oil-based adjuvants have been tested for human use. Typical adjuvants are Freund's complete adjuvant and Freund's incomplete adjuvant.

Suitable adjuvants that have been developed more recently, include liposomes, immune-stimulating complexes (ISCOMs), and squalene or squalene emulsions. Surface active agents having adjuvant activity can also be employed. These include saponin-like Quil A molecules in ISCOMs and Pluronic® block copolymers that are used to make sTable squalene emulsions. Saponins are surface-active agents widely distributed in plants.

Analogs of muramyl dipeptide (MDP) or muramyl tripeptide (MTP), such as threonine analog of MDP and lipopolysaccharide (LPS) having adjuvant activity and reduced side effects, are also suiTable for use as adjuvants. Synthetic analogs of MDP and the monophosphoryl derivative of lipid A are also known for their adjuvant activity and reduced pyrogenicity. A particularly suiTable formulation is Syntex Adjuvant Formulation-1 or SAF-1, which combines the threonyl analog of MDP in a vehicle comprised of Pluronic L-121 triblock polymer with squalene and a small proportion of Tween 80 as an emulsifying detergent. The preferred adjuvants for use in humans are MDP and its analogs, with or without squalene, saponins, and the monophosphoryl derivative of lipid A. When an adjuvant is combined with the immunogen in the composition and method of the invention, a further enhancement in immune response is observed.

A preferred route of administering the composition of the invention to a host is mucosal. Oral administration is the particularly preferred mode of administration because of its simplicity and because it is relatively non-invasive. It will be understood that the immunogenic composition of the invention can also

be employed in a vaccine. An alternative mucosal adjuvant could be used. All or part of the cholera (CT) or *E. coli* LT holotoxins in either toxic or detoxified forms are examples.

The composition of the invention can be incorporated into any suiTable delivery system. For example, the antigen and adjuvant can be combined with a pharmaceutically accepTable liquid vehicle, such as water, buffered saline, or edible animal or vegeTable oil. The composition can be combined with one or more suiTable pharmaceutically accepTable excipients or core materials, such as cellulose, cellulose derivatives, sucrose, gelatin, Starch 1500, NuTab, lactose, malto-dextrin, talc, Cabosil, magnesium stearate, alginate, Actisol, PEG 400, Myvacet, Triacetine, syrup, oil, sorbitol, mannitol, and Plasdone. This list is not intended to be exhaustive or limiting; alternative or additional excipients or core materials can also be used.

It will also be understood that the compositions of the invention can be formulated to include chemical agents that are capable of neutralizing stomach pH. Suitable neutralizing agents include H_2 antagonists, proton pump inhibitors, bicarbonate of soda, calcium carbonate, and aluminum hydroxide.

The composition of the invention can be utilized in the form of elixirs, solutions, suspensions, syrups, aerosols, and the like. The composition can also be prepared in dosage units suiTable for oral or parenteral administration, such as particles, granules, beads, tablets, hard gelatin capsules, and soft gelatin capsules.

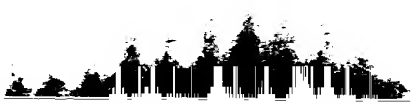
The immunogen and adjuvant are employed in a combined amount to provide an immune response against an infectious agent. This can be determined by estimating seroconversion, that is, the levels of antibody before and after immunization. If the host has a preexisting antibody titer to the antigen, the success of immunization can be determined by the extent of increase in the level of specific antibody. In cases where there is no correlation between

seroconversion and protection, cell-mediated immune response can be monitored.

The amount of antigen and adjuvant per dosage unit will depend on the desired dose and the frequency of administration. In one embodiment, each dosage unit contains an amount of antigen effective to protect the animal against disease following exposure to the pathogen. The dose can be defined as the amount of immunogen necessary to raise an immune response against *H. pylori* infection in an individual. As an example, the immunization schedule in animals (mice) consists of 4 administrations (one/week). Each oral dose unit (one per week) comprises 250 to 900 micrograms of UreB and 250 to 900 micrograms of HspA and 25 to 90 micrograms of adjuvant. A suiTable weight ratio of UreB:HspA:adjuvant is 1:1:0.1, but it will be understood that other ratios of ingredients can be employed. The average weight of a mouse is 20 g and one can calculate for one kilogram of other animal or a human patient to be immunized the equivalent dose unit. The precise composition will necessarily vary depending on the antigen and adjuvant selected, the species to be immunized, and other factors, and it is within the capacity of one with ordinary skill in the art to search for an optimal formulation.

The immunogenic composition can be administered before or after infection. A booster dose can comprise the antigen in an amount sufficient to enhance the initial immune response. It has to be adapted to each protocol depending on the antigen and the host. Multiple doses may be more appropriate for children and for individuals with no known prior exposure.

The immunogenic composition containing UreB and HspA can be administered to an infected or non-infected animal. Thus, it will be understood that this invention can be employed for the prophylactic, therapeutic, or curative treatment of any animal in need thereof, such as dogs, cats, poultry, pigs,



horses, and cattle, and especially mammals, such as primates, including humans, using UreB and HspA or the species equivalent thereof.

Finally, a preferred embodiment of the previously described antibodies of the invention comprises monoclonal antibodies, polyclonal antibodies, or fragments of such antibodies that immunologically recognize UreB, HspA, or mixtures of UreB and HspA. Antibodies and antibody fragments that are specific for these polypeptides and their immunologically recognizable fragments can be prepared by the techniques described above.

Inasmuch as the present invention is subject to many variations, modifications, and changes in details, it is intended that all subject matter discussed above or shown in the accompanying drawings be interpreted as illustrative and not in a limiting sense. Such modifications and variations are included within the scope of this invention as defined by the following claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: INSTITUT PASTEUR
(B) STREET: 25-28 rue du Dr Roux
(C) CITY: PARIS CEDEX 15
(E) COUNTRY: FRANCE
(F) POSTAL CODE (ZIP): 75724
(G) TELEPHONE: 45.68.80.94
(H) TELEFAX: 40.61.30.17

(A) NAME: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
(B) STREET: 101 rue de Tolbiac
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(E) COUNTRY: FRANCE
(F) POSTAL CODE (ZIP): 75654
(G) TELEPHONE: 44.23.60.00
(H) TELEFAX: 45.85.07.66

(ii) TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE COMPOSITIONS AND NUCLEIC ACID SEQUENCES ENCODING SAID POLYPEPTIDES.

(iii) NUMBER OF SEQUENCES: 19

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 94/01625

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP 93401309.5
(B) FILING DATE: 19-MAY-1993

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP 93/03259
(B) FILING DATE: 19-NOV-1993

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 31..36
(D) OTHER INFORMATION: /standard_name= "Shine-Dalgarno sequence"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 756..759
(D) OTHER INFORMATION: /standard_name= "Shine-Dalgarno sequence"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 43..753
(D) OTHER INFORMATION: /standard_name= "URE A - FIGURE 3"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 766..2475
(D) OTHER INFORMATION: /standard_name= "URE B - FIGURE 3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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                                                Met Lys Leu Thr
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CCT AAA GAA CTA GAC AAG TTA ATG CTC CAT TAT GCG GGC AGA TTG GCA         102
Pro Lys Glu Leu Asp Lys Leu Met Leu His Tyr Ala Gly Arg Leu Ala
  5                  10                  15                  20

GAA GAA CGC TTG GCG CGT GGT GTG AAA CTC AAT TAC ACC GAA GCG GTC         150
Glu Glu Arg Leu Ala Arg Gly Val Lys Leu Asn Tyr Thr Glu Ala Val
                 25                  30                  35

GCG CTC ATT AGC GGG CGT GTG ATG GAA AAG GCG CGT GAT GGT AAT AAA         198
Ala Leu Ile Ser Gly Arg Val Met Glu Lys Ala Arg Asp Gly Asn Lys
             40                  45                  50

AGC GTG GCG GAT TTG ATG CAA GAA GGC AGG ACT TGG CTT AAA AAA GAA         246
Ser Val Ala Asp Leu Met Gln Glu Gly Arg Thr Trp Leu Lys Lys Glu
         55                  60                  65
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AAT GTG ATG GAC GGC GTA GCA AGC ATG ATT CAT GAA GTG GGG ATT GAA          294
Asn Val Met Asp Gly Val Ala Ser Met Ile His Glu Val Gly Ile Glu
 70                  75                  80

GCT AAC TTC CCC GAT GGA ACC AAG CTT GTA ACT ATC CAC ACT CCG GTA          342
Ala Asn Phe Pro Asp Gly Thr Lys Leu Val Thr Ile His Thr Pro Val
 85                  90                  95                 100

GAG GAT AAT GGC AAA TTA GCC CCC GGC GAG GTC TTC TTA AAA AAT GAG          390
Glu Asp Asn Gly Lys Leu Ala Pro Gly Glu Val Phe Leu Lys Asn Glu
                105                 110                 115

GAC ATT ACT ATT AAC GCC GGC AAA GAA GCC ATT AGC TTG AAA GTG AAA          438
Asp Ile Thr Ile Asn Ala Gly Lys Glu Ala Ile Ser Leu Lys Val Lys
            120                 125                 130

AAT AAA GGC GAT CGT CCT GTG CAG GTG GGA TCA CAT TTC CAC TTC TTC          486
Asn Lys Gly Asp Arg Pro Val Gln Val Gly Ser His Phe His Phe Phe
        135                 140                 145

GAA GTG AAT AAG CTC TTG GAC TTC GAT CGC GCA AAA AGC TTT TGC AAA          534
Glu Val Asn Lys Leu Leu Asp Phe Asp Arg Ala Lys Ser Phe Cys Lys
    150                 155                 160

CGC CTA GAC ATT GCA TCT GGA ACA GCG GTG CGC TTT GAA CCC GGG GAG          582
Arg Leu Asp Ile Ala Ser Gly Thr Ala Val Arg Phe Glu Pro Gly Glu
165                 170                 175                 180

GAA AAA AGT GTG GAA CTC ATT GAC ATC GGC GGG AAT AAG CGC ATC TAT          630
Glu Lys Ser Val Glu Leu Ile Asp Ile Gly Gly Asn Lys Arg Ile Tyr
                185                 190                 195

GGC TTT AAT TCT TTG GTG GAT CGC CAA GCC GAT GCC GAT GGT AAA AAA          678
Gly Phe Asn Ser Leu Val Asp Arg Gln Ala Asp Ala Asp Gly Lys Lys
            200                 205                 210

CTC GGC TTA AAA CGC GCT AAA GAA AAA GGT TTT GGG TCT GTA AAC TGC          726
Leu Gly Leu Lys Arg Ala Lys Glu Lys Gly Phe Gly Ser Val Asn Cys
        215                 220                 225

GGT TGT GAA GCG ACT AAA GAT AAA CAA TAAGGAAAAA CC ATG AAA AAG            774
Gly Cys Glu Ala Thr Lys Asp Lys Gln                 Met Lys Lys
    230                 235                             1

ATT TCA CGA AAA GAA TAT GTT TCT ATG TAT GGT CCC ACT ACC GGG GAT          822
Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr Thr Gly Asp
      5                  10                  15

CGT GTT AGA CTC GGC GAC ACT GAT TTG ATC TTA GAA GTG GAG CAT GAT          870
Arg Val Arg Leu Gly Asp Thr Asp Leu Ile Leu Glu Val Glu His Asp
 20                  25                  30                 35

TGC ACC ACT TAT GGT GAA GAG ATC AAA TTT GGG GGC GGT AAA ACT ATC          918
Cys Thr Thr Tyr Gly Glu Glu Ile Lys Phe Gly Gly Gly Lys Thr Ile
                40                  45                  50
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CGT GAT GGG ATG AGT CAA ACC AAT AGC CCT AGC TCT TAT GAA TTA GAT      966
Arg Asp Gly Met Ser Gln Thr Asn Ser Pro Ser Ser Tyr Glu Leu Asp
            55                  60                  65

TTG GTG CTC ACT AAC GCC CTC ATT GTG GAC TAT ACG GGC ATT TAC AAA     1014
Leu Val Leu Thr Asn Ala Leu Ile Val Asp Tyr Thr Gly Ile Tyr Lys
        70                  75                  80

GCC GAC ATT GGG ATT AAA GAC GGC AAG ATT GCA GGC ATT GGC AAG GCA     1062
Ala Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile Gly Lys Ala
    85                  90                  95

GGC AAT AAG GAC ATG CAA GAT GGC GTA GAT AAT AAT CTT TGC GTA GGT     1110
Gly Asn Lys Asp Met Gln Asp Gly Val Asp Asn Asn Leu Cys Val Gly
100                 105                 110                 115

CCT GCT ACA GAG GCT TTG GCA GCT GAG GGC TTG ATT GTA ACC GCT GGT     1158
Pro Ala Thr Glu Ala Leu Ala Ala Glu Gly Leu Ile Val Thr Ala Gly
                120                 125                 130

GGC ATC GAT ACG CAT ATT CAC TTT ATC TCT CCC CAA CAA ATC CCT ACT     1206
Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln Ile Pro Thr
            135                 140                 145

GCT TTT GCC AGC GGG GTT ACA ACC ATG ATT GGA GGA GGC ACA GGA CCT     1254
Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly Thr Gly Pro
        150                 155                 160

GCG GAT GGC ACG AAT GCG ACC ACC ATC ACT CCC GGA CGC GCT AAT CTA     1302
Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg Ala Asn Leu
    165                 170                 175

AAA AGT ATG TTG CGT GCA GCC GAA GAA TAC GCC ATG AAT CTA GGC TTT     1350
Lys Ser Met Leu Arg Ala Ala Glu Glu Tyr Ala Met Asn Leu Gly Phe
180                 185                 190                 195

TTG GCT AAG GGG AAT GTG TCT TAC GAA CCC TCT TTA CGC GAT CAG ATT     1398
Leu Ala Lys Gly Asn Val Ser Tyr Glu Pro Ser Leu Arg Asp Gln Ile
                200                 205                 210

GAA GCA GGG GCG ATT GGT TTT AAA ATC CAC GAA GAC TGG GGA AGC ACA     1446
Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp Gly Ser Thr
            215                 220                 225

CCT GCA GCT ATT CAC CAC TGC CTC AAT GTC GCC GAT GAA TAC GAT GTG     1494
Pro Ala Ala Ile His His Cys Leu Asn Val Ala Asp Glu Tyr Asp Val
        230                 235                 240

CAA GTG GCT ATC CAC ACC GAT ACC CTT AAC GAG GCG GGC TGT GTA GAA     1542
Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly Cys Val Glu
    245                 250                 255

GAC ACC CTA GAG GCG ATT GCC GGG CGC ACC ATC CAT ACC TTC CAC ACT     1590
Asp Thr Leu Glu Ala Ile Ala Gly Arg Thr Ile His Thr Phe His Thr
260                 265                 270                 275
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GAA GGG GCT GGG GGT GGA CAC GCT CCA GAT GTT ATC AAA ATG GCA GGG      1638
Glu Gly Ala Gly Gly Gly His Ala Pro Asp Val Ile Lys Met Ala Gly
                280                 285                 290

GAA TTT AAC ATT CTA CCC GCC TCT ACT AAC CCG ACC ATT CCT TTC ACC      1686
Glu Phe Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile Pro Phe Thr
            295                 300                 305

AAA AAC ACT GAA GCC GAG CAC ATG GAC ATG TTA ATG GTG TGC CAC CAC      1734
Lys Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val Cys His His
        310                 315                 320

TTG GAT AAA AGT ATC AAG GAA GAT GTG CAG TTT GCC GAT TCG AGG ATT      1782
Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp Ser Arg Ile
    325                 330                 335

CGC CCC CAA ACT ATC GCG GCT GAA GAC CAA CTC CAT GAC ATG GGG ATC      1830
Arg Pro Gln Thr Ile Ala Ala Glu Asp Gln Leu His Asp Met Gly Ile
340                 345                 350                 355

TTT TCT ATC ACC AGC TCC GAC TCT CAG GCT ATG GGA CGC GTA GGC GAG      1878
Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Val Gly Glu
                360                 365                 370

GTG ATC ACA CGC ACT TGG CAG ACA GCA GAC AAA AAC AAA AAA GAG TTT      1926
Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys Glu Phe
            375                 380                 385

GGG CGC TTG AAA GAG GAA AAA GGC GAT AAC GAC AAC TTC CGC ATC AAA      1974
Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe Arg Ile Lys
        390                 395                 400

CGC TAC ATC TCT AAA TAC ACC ATC AAC CCC GGG ATC GCG CAT GGG ATT      2022
Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Gly Ile Ala His Gly Ile
    405                 410                 415

TCT GAC TAT GTG GGC TCT GTG GAA GTG GGC AAA TAC GCC GAC CTC GTG      2070
Ser Asp Tyr Val Gly Ser Val Glu Val Gly Lys Tyr Ala Asp Leu Val
420                 425                 430                 435

CTT TGG AGT CCG GCT TTC TTT GGC ATT AAG CCC AAT ATG ATT ATT AAG      2118
Leu Trp Ser Pro Ala Phe Phe Gly Ile Lys Pro Asn Met Ile Ile Lys
                440                 445                 450

GGC GGA TTT ATT GCG CTC TCT CAA ATG GGC GAT GCC AAT GCG TCT ATT      2166
Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn Ala Ser Ile
            455                 460                 465

CCC ACC CCT CAG CCC GTC TAT TAC CGT GAA ATG TTT GGA CAC CAT GGG      2214
Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His His Gly
        470                 475                 480

AAA AAC AAA TTC GAC ACC AAT ATC ACT TTC GTG TCC CAA GCG GCT TAC      2262
Lys Asn Lys Phe Asp Thr Asn Ile Thr Phe Val Ser Gln Ala Ala Tyr
    485                 490                 495
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AAG GCA GGG ATC AAA GAA GAA CTA GGG CTA GAT CGC GCG GCA CCG CCA      2310
Lys Ala Gly Ile Lys Glu Glu Leu Gly Leu Asp Arg Ala Ala Pro Pro
500                 505                 510                 515

GTG AAA AAC TGT CGC AAT ATC ACT AAA AAG GAC CTC AAA TTC AAC GAT      2358
Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Leu Lys Phe Asn Asp
                520                 525                 530

GTG ACC GCA CAT ATT GAT GTC AAC CCT GAA ACC TAT AAG GTG AAA GTG      2406
Val Thr Ala His Ile Asp Val Asn Pro Glu Thr Tyr Lys Val Lys Val
            535                 540                 545

GAT GGC AAA GAG GTA ACC TCT AAA GCA GCA GAT GAA TTG AGC CTA GCG      2454
Asp Gly Lys Glu Val Thr Ser Lys Ala Ala Asp Glu Leu Ser Leu Ala
        550                 555                 560

CAA CTT TAT AAT TTG TTC TGGAGGCTA AGGAGGGGGA TAGAGGGGGT             2502
Gln Leu Tyr Asn Leu Phe
    565                 570

TTATTTAGAG GGGAGTCATT GATTTACCTT TGCTAGTTTA TAATGGATTT AAGAGAGGTT    2562

TTTTTTCGTG TTTTATACCG CGTTGAAACC CTCAAATCTT TACCAAAAGG ATGGTAA      2619
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter felis

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..237
(D) OTHER INFORMATION: /note= "Corresponds to figure 4, line 1 (ure A)."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Lys Leu Thr Pro Lys Glu Leu Asp Lys Leu Met Leu His Tyr Ala
1               5                   10                  15

Gly Arg Leu Ala Glu Glu Arg Leu Ala Arg Gly Val Lys Leu Asn Tyr
            20                  25                  30

Thr Glu Ala Val Ala Leu Ile Ser Gly Arg Val Met Glu Lys Ala Arg
        35                  40                  45
```

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Asp Gly Asn Lys Ser Val Ala Asp Leu Met Gln Glu Gly Arg Thr Trp
     50                  55                  60

Leu Lys Lys Glu Asn Val Met Asp Gly Val Ala Ser Met Ile His Glu
65                  70                  75                  80

Val Gly Ile Glu Ala Asn Phe Pro Asp Gly Thr Lys Leu Val Thr Ile
                85                  90                  95

His Thr Pro Val Glu Asp Asn Gly Lys Leu Ala Pro Gly Glu Val Phe
            100                 105                 110

Leu Lys Asn Glu Asp Ile Thr Ile Asn Ala Gly Lys Glu Ala Ile Ser
        115                 120                 125

Leu Lys Val Lys Asn Lys Gly Asp Arg Pro Val Gln Val Gly Ser His
    130                 135                 140

Phe His Phe Phe Glu Val Asn Lys Leu Leu Asp Phe Asp Arg Ala Lys
145                 150                 155                 160

Ser Phe Cys Lys Arg Leu Asp Ile Ala Ser Gly Thr Ala Val Arg Phe
                165                 170                 175

Glu Pro Gly Glu Glu Lys Ser Val Glu Leu Ile Asp Ile Gly Gly Asn
            180                 185                 190

Lys Arg Ile Tyr Gly Phe Asn Ser Leu Val Asp Arg Gln Ala Asp Ala
        195                 200                 205

Asp Gly Lys Lys Leu Gly Leu Lys Arg Ala Lys Glu Lys Gly Phe Gly
    210                 215                 220

Ser Val Asn Cys Gly Cys Glu Ala Thr Lys Asp Lys Gln
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter felis

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..569
(D) OTHER INFORMATION: /note= "Corresponds to figure 4, line 1 (ure B)."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Lys Ile Ser Arg Lys Glu Tyr Val Ser Met Tyr Gly Pro Thr
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Thr Gly Asp Arg Val Arg Le Asp Leu Ile Leu Glu Val
20 30

Glu His Asp Cys Thr Thr Tyr Gly G Lys Phe Gly Gly Gly
35 40 45

hr Ile Arg Asp Gly Met Ser Gln Thr ro Ser Ser Tyr
55

sp Leu Val Leu Thr Asn Ala Leu Ile Va Tyr Thr Gly
70 75 80

Ile a Asp Ile Gly Ile Lys Asp Gly Lys Ile Ala Gly Ile
85 90 95

Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Asp Asn Asn Leu
100 105 110

Cys Val Gly Pro Ala Thr Glu Ala Leu Ala Ala Glu Gly Leu Ile Val
115 120 125

Thr Ala Gly Gly Ile Asp Thr His Ile His Phe Ile Ser Pro Gln Gln
130 135 140

Ile Pro Thr Ala Phe Ala Ser Gly Val Thr Thr Met Ile Gly Gly Gly
145 150 155 160

Thr Gly Pro Ala Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Arg
165 170 175

Ala Asn Leu Lys Ser Met Leu Arg Ala Ala Glu Glu Tyr Ala Met Asn
180 185 190

Leu Gly Phe Leu Ala Lys Gly Asn Val Ser Tyr Glu Pro Ser Leu Arg
195 200 205

Asp Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Ile His Glu Asp Trp
210 215 220

Gly Ser Thr Pro Ala Ala Ile His His Cys Leu Asn Val Ala Asp Glu
225 230 235 240

Tyr Asp Val Gln Val Ala Ile His Thr Asp Thr Leu Asn Glu Ala Gly
245 250 255

Cys Val Glu Asp Thr Leu Glu Ala Ile Ala Gly Arg Thr Ile His Thr
260 265 270

Phe His Thr Glu Gly Ala Gly Gly Gly His Ala Pro Asp Val Ile Lys
275 280 285

Met Ala Gly Glu Phe Asn Ile Leu Pro Ala Ser Thr Asn Pro Thr Ile
290 295 300

Pro Phe Thr Lys Asn Thr Glu Ala Glu His Met Asp Met Leu Met Val
305 310 315 320

Cys His His Leu Asp Lys Ser Ile Lys Glu Asp Val Gln Phe Ala Asp
325 330 335

Ser Arg Ile Arg Pro Gln Thr Ile Ala Ala Glu Asp Gln Leu His Asp
340 345 350

Met Gly Ile Phe Ser Ile Thr Ser Ser Asp Ser Gln Ala Met Gly Arg
355 360 365

Val Gly Glu Val Ile Thr Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys
370 375 380

Lys Glu Phe Gly Arg Leu Lys Glu Glu Lys Gly Asp Asn Asp Asn Phe
385 390 395 400

Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Gly Ile Ala
405 410 415

His Gly Ile Ser Asp Tyr Val Gly Ser Val Glu Val Gly Lys Tyr Ala
420 425 430

Asp Leu Val Leu Trp Ser Pro Ala Phe Phe Gly Ile Lys Pro Asn Met
435 440 445

Ile Ile Lys Gly Gly Phe Ile Ala Leu Ser Gln Met Gly Asp Ala Asn
450 455 460

Ala Ser Ile Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly
465 470 475 480

His His Gly Lys Asn Lys Phe Asp Thr Asn Ile Thr Phe Val Ser Gln
485 490 495

Ala Ala Tyr Lys Ala Gly Ile Lys Glu Glu Leu Gly Leu Asp Arg Ala
500 505 510

Ala Pro Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Leu Lys
515 520 525

Phe Asn Asp Val Thr Ala His Ile Asp Val Asn Pro Glu Thr Tyr Lys
530 535 540

Val Lys Val Asp Gly Lys Glu Val Thr Ser Lys Ala Ala Asp Glu Leu
545 550 555 560

Ser Leu Ala Gln Leu Tyr Asn Leu Phe
565

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2284 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 124..477
(D) OTHER INFORMATION: /standard_name= "H. pylori - Hsp A"

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 506..2143
(D) OTHER INFORMATION: /standard_name= "H. pylori - Hsp B"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..2284
(D) OTHER INFORMATION: /note= "Corresponds to figure 6."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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GAA ATG AAG TTT CAA CCA TTA GGA GAA AGG GTC TTA GTA GAA AGA CTT        168
    Met Lys Phe Gln Pro Leu Gly Glu Arg Val Leu Val Glu Arg Leu
      1               5                  10                  15

GAA GAA GAG AAC AAA ACC AGT TCA GGC ATC ATC ATC CCT GAT AAC GCT        216
Glu Glu Glu Asn Lys Thr Ser Ser Gly Ile Ile Ile Pro Asp Asn Ala
                  20                  25                  30

AAA GAA AAG CCT TTA ATG GGC GTA GTC AAA GCG GTT AGC CAT AAA ATC        264
Lys Glu Lys Pro Leu Met Gly Val Val Lys Ala Val Ser His Lys Ile
              35                  40                  45

AGT GAG GGT TGC AAA TGC GTT AAA GAA GGC GAT GTG ATC GCT TTT GGC        312
Ser Glu Gly Cys Lys Cys Val Lys Glu Gly Asp Val Ile Ala Phe Gly
          50                  55                  60

AAA TAC AAA GGC GCA GAA ATC GTT TTA GAT GGC GTT GAA TAC ATG GTG        360
Lys Tyr Lys Gly Ala Glu Ile Val Leu Asp Gly Val Glu Tyr Met Val
      65                  70                  75

CTA GAA CTA GAA GAC ATT CTA GGT ATT GTG GGC TCA GGC TCT TGC TGT        408
Leu Glu Leu Glu Asp Ile Leu Gly Ile Val Gly Ser Gly Ser Cys Cys
  80                  85                  90                  95
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CAT ACA GGT AAT CAT GAT CAT AAA CAT GCT AAA GAG CAT GAA GCT TGC          456
His Thr Gly Asn His Asp His Lys His Ala Lys Glu His Glu Ala Cys
                100                 105                 110

TGT CAT GAT CAC AAA AAA CAC TAAAAAACAT TATTATTAAG GATACAAA ATG          508
Cys His Asp His Lys Lys His                                 Met
            115                                               1

GCA AAA GAA ATC AAA TTT TCA GAT AGC GCA AGA AAC CTT TTA TTT GAA          556
Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe Glu
              5                  10                  15

GGC GTA AGA CAA CTC CAT GAC GCT GTC AAA GTA ACC ATG GGG CCA AGA          604
Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro Arg
         20                  25                  30

GGC AGG AAC GTG TTG ATC CAA AAA AGC TAT GGC GCT CCA AGC ATC ACC          652
Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile Thr
     35                  40                  45

AAA GAC GGC GTG AGC GTG GCT AAA GAG ATT GAA TTA AGT TGC CCC GTG          700
Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro Val
 50                  55                  60                  65

GCT AAC ATG GGC GCT CAG CTC GTT AAA GAA GAT GCG AGC AAA ACC GCT          748
Ala Asn Met Gly Ala Gln Leu Val Lys Glu Asp Ala Ser Lys Thr Ala
                70                  75                  80

GAT GCC GCC GGC GAT GGC ACG ACC ACA GCG ACC GTG CTG GCT TAT AGC          796
Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr Ser
            85                  90                  95

ATT TTT AAA GAG GGC TTG AGG AAT ATC ACG GCT GGG GCT AAC CCT ATT          844
Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro Ile
        100                 105                 110

GAA GTG AAA CGA GGC ATG GAT AAA GCG CCT GAA GCG ATC ATT AAT GAG          892
Glu Val Lys Arg Gly Met Asp Lys Ala Pro Glu Ala Ile Ile Asn Glu
    115                 120                 125

CTT AAA AAA GCG AGC AAA AAA GTG GGC GGT AAA GAA GAA ATC ACC CAA          940
Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr Gln
130                 135                 140                 145

GTA GCG ACC ATT TCT GCA AAC TCC GAT CAC AAT ATC GGG AAA CTC ATC          988
Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu Ile
                150                 155                 160

GCT GAC GCT ATG GAA AAA GTG GGT AAA GAC GGC GTG ATC ACC GTT GAA         1036
Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val Glu
            165                 170                 175

GAA GCT AAG GGC ATT GAA GAT GAA TTA GAT GTC GTA GAA GGC ATG CAA         1084
Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met Gln
        180                 185                 190
```

```
TTT GAT AGA GGC TAC CTC TCC CCT TAC TTT GTA ACC AAC GCT GAG AAA      1132
Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu Lys
    195                 200                 205

ATG ACC GCT CAA TTG GAT AAC GCT TAC ATC CTT TTA ACG GAT AAA AAA      1180
Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys Lys
                215                 220                 225

[illegible]C ATG AAA GAC ATT CTC CCG CTA CTA GAA AAA ACC ATG AAA      1228
[illegible]  Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met Lys
             230                 235                 240

GAG GGC [illegible]TT TTA ATC ATC GCT GAA GAC ATT GAG GGC GAA GCT      1276
Glu Gly Ly[illegible]u Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu Ala
                        250                 255

TTA ACG ACT CTA GTG GTG AAT AAA TTA AGA GGC GTG TTG AAT ATC GCA      1324
Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile Ala
        260                 265                 270

GCG GTT AAA GCT CCA GGC TTT GGG GAC AGG AGA AAA GAA ATG CTC AAA      1372
Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu Lys
    275                 280                 285

GAC ATC GCT GTT TTA ACC GGC GGT CAA GTC ATT AGC GAA GAA TTG GGC      1420
Asp Ile Ala Val Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu Gly
290                 295                 300                 305

TTG AGT CTA GAA AAC GCT GAA GTG GAG TTT TTA GGC AAA GCG AAG ATT      1468
Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Lys Ile
                310                 315                 320

GTG ATT GAC AAA GAC AAC ACC ACG ATC GTA GAT GGC AAA GGC CAT AGC      1516
Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly His Ser
            325                 330                 335

CAT GAC GTC AAA GAC AGA GTC GCG CAA ATC AAA ACC CAA ATT GCA AGC      1564
His Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile Ala Ser
        340                 345                 350

ACG ACA AGC GAT TAC GAC AAA GAA AAA TTG CAA GAA AGA TTG GCC AAA      1612
Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala Lys
    355                 360                 365

CTC TCT GGC GGT GTG GCT GTG ATT AAA GTG GGC GCT GCG AGT GAA GTG      1660
Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser Glu Val
370                 375                 380                 385

GAA ATG AAA GAG AAA AAA GAC CGG GTG GAT GAC GCG TTG AGC GCG ACT      1708
Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser Ala Thr
                390                 395                 400

AAA GCG GCG GTT GAA GAA GGC ATT GTG ATT GGG GGC GGT GCG GCC CTC      1756
Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala Ala Leu
            405                 410                 415
```

```
ATT CGC GCG GCC CAA AAA GTG CAT TTG AAT TTA CAC GAT GAT GAA AAA      1804
Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp Glu Lys
        420                 425                 430

GTG GGC TAT GAA ATC ATC ATG CGC GCC ATT AAA GCC CCA TTA GCT CAA      1852
Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu Ala Gln
    435                 440                 445

ATC GCT ATC AAT GCC GGT TAT GAT GGC GGT GTG GTC GTG AAT GAA GTA      1900
Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn Glu Val
450                 455                 460                 465

GAA AAA CAC GAA GGG CAT TTT GGT TTT AAC GCT AGC AAT GGC AAG TAT      1948
Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly Lys Tyr
                470                 475                 480

GTG GAC ATG TTT AAA GAA GGC ATT ATT GAC CCC TTA AAA GTA GAA AGG      1996
Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val Glu Arg
            485                 490                 495

ATC GCT TTA CAA AAT GCG GTT TCG GTT TCA AGC CTG CTT TTA ACC ACA      2044
Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu Thr Thr
        500                 505                 510

GAA GCC ACC GTG CAT GAA ATC AAA GAA GAA AAA GCG GCC CCA GCA ATG      2092
Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Ala Pro Ala Met
    515                 520                 525

CCT GAT ATG GGT GGC ATG GGC GGA ATG GGA GGC ATG GGC GGC ATG ATG      2140
Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Met
530                 535                 540                 545

TAAGCCCCCT TGCTTTTTGG TATCATCTGC TTTTAAAATC CATCTTCTAG AATCCCCCCT    2200

TCTAAAATCC CTTTTTTGGG GGGTGCTTTT GGTTTGATAA AACCGCTCGC TTTTAAAAAC    2260

GCGCAACAAA AAACTCTGTT AAGC                                           2284
```

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 545 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..545
(D) OTHER INFORMATION: /note= "Corresponds to figure 7A"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
Met Ala Lys Glu Ile Lys Phe Ser Asp Ser Ala Arg Asn Leu Leu Phe
 1               5                  10                  15

Glu Gly Val Arg Gln Leu His Asp Ala Val Lys Val Thr Met Gly Pro
            20                  25                  30

Arg Gly Arg Asn Val Leu Ile Gln Lys Ser Tyr Gly Ala Pro Ser Ile
        35                  40                  45

Thr Lys Asp Gly Val Ser Val Ala Lys Glu Ile Glu Leu Ser Cys Pro
    50                  55                  60

Val Ala Asn Met Gly Ala Gln Leu Val Lys Glu Asp Ala Ser Lys Thr
65                  70                  75                  80

Ala Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Tyr
                85                  90                  95

Ser Ile Phe Lys Glu Gly Leu Arg Asn Ile Thr Ala Gly Ala Asn Pro
            100                 105                 110

Ile Glu Val Lys Arg Gly Met Asp Lys Ala Pro Glu Ala Ile Ile Asn
        115                 120                 125

Glu Leu Lys Lys Ala Ser Lys Lys Val Gly Gly Lys Glu Glu Ile Thr
    130                 135                 140

Gln Val Ala Thr Ile Ser Ala Asn Ser Asp His Asn Ile Gly Lys Leu
145                 150                 155                 160

Ile Ala Asp Ala Met Glu Lys Val Gly Lys Asp Gly Val Ile Thr Val
                165                 170                 175

Glu Glu Ala Lys Gly Ile Glu Asp Glu Leu Asp Val Val Glu Gly Met
            180                 185                 190

Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Val Thr Asn Ala Glu
        195                 200                 205

Lys Met Thr Ala Gln Leu Asp Asn Ala Tyr Ile Leu Leu Thr Asp Lys
    210                 215                 220

Lys Ile Ser Ser Met Lys Asp Ile Leu Pro Leu Leu Glu Lys Thr Met
225                 230                 235                 240

Lys Glu Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Ile Glu Gly Glu
                245                 250                 255

Ala Leu Thr Thr Leu Val Val Asn Lys Leu Arg Gly Val Leu Asn Ile
            260                 265                 270

Ala Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Glu Met Leu
        275                 280                 285

Lys Asp Ile Ala Val Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Leu
    290                 295                 300
```

```
Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Lys
305                 310                 315                 320

Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly His
                325                 330                 335

Ser His Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile Ala
            340                 345                 350

Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu Ala
        355                 360                 365

Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser Glu
    370                 375                 380

Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser Ala
385                 390                 395                 400

Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala Ala
                405                 410                 415

Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp Glu
            420                 425                 430

Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu Ala
        435                 440                 445

Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn Glu
    450                 455                 460

Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly Lys
465                 470                 475                 480

Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val Glu
                485                 490                 495

Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu Thr
            500                 505                 510

Thr Glu Ala Thr Val His Glu Ile Lys Glu Glu Lys Ala Ala Pro Ala
        515                 520                 525

Met Pro Asp Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Met
    530                 535                 540

Met
545
```

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..118
(D) OTHER INFORMATION: /note= "Corresponds to figure 7B."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Lys Phe Gln Pro Leu Gly Glu Arg Val Leu Val Glu Arg Leu Glu
 1               5                  10                  15

Glu Glu Asn Lys Thr Ser Ser Gly Ile Ile Ile Pro Asp Asn Ala Lys
            20                  25                  30

Glu Lys Pro Leu Met Gly Val Val Lys Ala Val Ser His Lys Ile Ser
        35                  40                  45

Glu Gly Cys Lys Cys Val Lys Glu Gly Asp Val Ile Ala Phe Gly Lys
    50                  55                  60

Tyr Lys Gly Ala Glu Ile Val Leu Asp Gly Val Glu Tyr Met Val Leu
65                  70                  75                  80

Glu Leu Glu Asp Ile Leu Gly Ile Val Gly Ser Gly Ser Cys Cys His
                85                  90                  95

Thr Gly Asn His Asp His Lys His Ala Lys Glu His Glu Ala Cys Cys
            100                 105                 110

His Asp His Lys Lys His
        115
```

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: H. felis

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..591
(D) OTHER INFORMATION: /standard_name= "URE I"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..591
(D) OTHER INFORMATION: /note= "Corresponds to figure 9."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```
ATG TTA GGT CTT GTG TTA TTG TAT GTT GCG GTC GTG CTG ATC AGC AAC        48
Met Leu Gly Leu Val Leu Leu Tyr Val Ala Val Val Leu Ile Ser Asn
  1               5                  10                  15

GGA GTT AGT GGG CTT GCA AAT GTG GAT GCC AAA AGC AAA GCC ATC ATG        96
Gly Val Ser Gly Leu Ala Asn Val Asp Ala Lys Ser Lys Ala Ile Met
            20                  25                  30

AAC TAC TTT GTG GGG GGG GAC TCT CCA TTG TGT GTA ATG TGG TCG CTA       144
Asn Tyr Phe Val Gly Gly Asp Ser Pro Leu Cys Val Met Trp Ser Leu
        35                  40                  45

TCA TCT TAT TCC ACT TTC CAC CCC ACC CCC CCT GCA ACT GGT CCA GAA       192
Ser Ser Tyr Ser Thr Phe His Pro Thr Pro Pro Ala Thr Gly Pro Glu
    50                  55                  60

GAT GTC GCG CAG GTG TCT CAA CAC CTC ATT AAC TTC TAT GGT CCA GCG       240
Asp Val Ala Gln Val Ser Gln His Leu Ile Asn Phe Tyr Gly Pro Ala
65                  70                  75                  80

ACT GGT CTA TTG TTT GGT TTT ACC TAC TTG TAT GCT GCC ATC AAC AAC       288
Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn Asn
                85                  90                  95

ACT TTC AAT CTC GAT TGG AAA CCC TAT GGC TGG TAT TGC TTG TTT GTA       336
Thr Phe Asn Leu Asp Trp Lys Pro Tyr Gly Trp Tyr Cys Leu Phe Val
            100                 105                 110

ACC ATC AAC ACT ATC CCA GCG GCC ATT CTT TCT CAC TAT TCC GAT GCG       384
Thr Ile Asn Thr Ile Pro Ala Ala Ile Leu Ser His Tyr Ser Asp Ala
        115                 120                 125

CTT GAT GAT CAC CGC CTC TTA GGA ATC ACT GAG GGC GAT TGG TGG GCT       432
Leu Asp Asp His Arg Leu Leu Gly Ile Thr Glu Gly Asp Trp Trp Ala
    130                 135                 140

TTC ATT TGG CTT GCT TGG GGT GTT TTG TGG CTC ACT GGT TGG ATT GAA       480
Phe Ile Trp Leu Ala Trp Gly Val Leu Trp Leu Thr Gly Trp Ile Glu
145                 150                 155                 160

TGC GCA CTT GGT AAG AGT CTA GGT AAA TTT GTT CCA TGG CTT GCC ATC       528
Cys Ala Leu Gly Lys Ser Leu Gly Lys Phe Val Pro Trp Leu Ala Ile
                165                 170                 175

GTC GAG GGC GTG ATC ACC GCT TGG ATT CCT GCT TGG CTA CTC TTT ATC       576
Val Glu Gly Val Ile Thr Ala Trp Ile Pro Ala Trp Leu Leu Phe Ile
            180                 185                 190
```

CAA CAC TGG TCT TGA 591
Gln His Trp Ser
195

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: H. felis

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..199
(D) OTHER INFORMATION: /note= "Corresponds to figure 10."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Lys Gly Trp Met Leu Gly Leu Val Leu Leu Tyr Val Ala Val Val Leu
1 5 10 15

Ile Ser Asn Gly Val Ser Gly Leu Ala Asn Val Asp Ala Lys Ser Lys
20 25 30

Ala Ile Met Asn Tyr Phe Val Gly Gly Asp Ser Pro Leu Cys Val Met
35 40 45

Trp Ser Leu Ser Ser Tyr Ser Thr Phe His Pro Thr Pro Pro Ala Thr
50 55 60

Gly Pro Glu Asp Val Ala Gln Val Ser Gln His Leu Ile Asn Phe Tyr
65 70 75 80

Gly Pro Ala Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala
85 90 95

Ile Asn Asn Thr Phe Asn Leu Asp Trp Lys Pro Tyr Gly Trp Tyr Cys
100 105 110

Leu Phe Val Thr Ile Asn Thr Ile Pro Ala Ala Ile Leu Ser His Tyr
115 120 125

Ser Asp Ala Leu Asp Asp His Arg Leu Leu Gly Ile Thr Glu Gly Asp
130 135 140

Trp Trp Ala Phe Ile Trp Leu Ala Trp Gly Val Leu Trp Leu Thr Gly
145 150 155 160

Trp Ile Glu Cys Ala Leu Gly Lys Ser Leu Gly Lys Phe Val Pro Trp
165 170 175

Leu Ala Ile Val Glu Gly Val Ile Thr Ala Trp Ile Pro Ala Trp Leu
180 185 190

Leu Phe Ile Gln His Trp Ser
195

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: H. pylori

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /note= "Corresponds to sequence mentioned at page 13 of the description."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Gly Ser Cys Cys His Thr Gly Asn His Asp His Lys His Ala Lys Glu
1 5 10 15

His Glu Ala Cys Cys His Asp His Lys Lys His
20 25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /note= "Corresponds to primer 1F of table 2 (page 51)."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CAUCCNAARG ARYTNGAYAA RYTNATC 27

(2) INFORMATION FOR SEQ ID NO: 1

(i EQUENCE CHARACTERISTICS:
A) LENGTH: 30 base pairs
B) TYPE: nucleic acid
) STRANDEDNESS: double
TOPOLOGY: unknown

ULE TYPE: DNA (genomic)

E:
AME/KEY: misc_feature
CATION: 1..30
ER INFORMATION: /note= "Corresponds to primer 1R of table 2 (page 51)."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

YTCYTTNCGN GGNSWDATYT TYTTCATCUA 30

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /note= "Corresponds to primer 2F of table 2 (page 51 of the description)."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..11
(D) OTHER INFORMATION: /note= "Restriction site introduced in the amplified fragment (EcoRI)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCGGAGAATT CATTAGCAGA AAAGAATATG TTTCTATG 38

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /note= "Corresponds to primer 2R of table 2 (page 51)."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..11
(D) OTHER INFORMATION: /note= "Restriction site introduced in the amplified fragment (PstI)."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ACGTTCTGCA GCTTACGAAT AACTTTTGTT GCTTGAGC 38

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /note= "Corresponds to primer 3F of table 2 (page 51)."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..6
(D) OTHER INFORMATION: /note= "Restriction site introduced in the amplified fragment (BamHI)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAAAA AGATTTCACG 20

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE [illegible]TICS:
(A) LEN[illegible] pairs
(B) TYPE: [illegible]
(C) STRAN[illegible]e
(D) TOPOLO[illegible]

ii) MOLECULE TYPE: D[illegible])

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..30
(D) OTHER INFORMATION: /note= "Corresponds to primer 3R of table 2 (page 51)."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 3..8
(D) OTHER INFORMATION: /note= "Restriction site introduced in the amplified fragment (HindIII)"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 9..14
(D) OTHER INFORMATION: /note= "Restriction site introduced in the amplified fragment (PstI)."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGAAGCTTCT GCAGGTGTGC TTCCCCAGTC 30

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /note= "Corresponds to oligo 1 of page 69."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..11
(D) OTHER INFORMATION: /note= "restriction site EcoRI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCGGAGAATT CAAGTTTCAA CCATTAGGAG AAAGGGTC 38

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /note= "Corresponds to oligo 2 of page 69."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..11
(D) OTHER INFORMATION: /note= "Restriction site PstI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ACGTTCTGCA GTTTAGTGTT TTTTGTGATC ATGACAGC 38

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /note= "Corresponds to oligo 3 of page 69."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..11
(D) OTHER INFORMATION: /note= "Restriction site EcoRI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CCGGAGAATT CGCAAAAGAA ATCAAATTTT CAGATAGC 38

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..38
(D) OTHER INFORMATION: /note= "Corresponds to oligo 4 of page 69."

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6..11
(D) OTHER INFORMATION: /note= "Restriction site PstI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACGTTCTGCA GATGATACCA AAAAGCAAGG GGGCTTAC 38

CLAIMS

1. A composition comprising a mixture of antigens of Helicobacter wherein said mixture consists essentially of UreB and HspA of H. pylori or polypeptides having at least 75 % and preferably 80 to 90 % similarity with said UreB or HspA, or fragments thereof capable of eliciting antibodies recognized by H. pylori, or an immune cellular response against an H.pylori infection .

2. A composition according to Claim 1 wherein said mixture consists essentially of UreB and HspA of H. felis or polypeptides having at least 75% and preferably 80 to 90 % similarity with said UreB or HspA, or fragments thereof capable of inducing antibodies recognized by H. pylori or an immune cellular response against an H. pylori infection.

3. A composition according to claim 1 or claim 2, wherein said HspA fragment is the C-terminal sequence of HspA of H. pylori replying to or included in the following amino-acid sequence :

G S C C H T G N H D H K H A K E H E A C C H D H K K H.

4. A composition according to anyone of claims 1 to 3 wherein the amount of antigens or polypeptides having at least 75 % and preferably 80 to 90 % similarity with said UreB or HspA, or fragments thereof is sufficient to elicit an immune response in a host to whom it is administered.

5. A composition according to anyone of claims 1 to 4 wherein the fragments comprise between 9 and 200 aminoacid residues and are in an amount sufficient to elicit an immune response in a host to whom it is administered

6. A composition according to anyone of claims 1 to 5, characterized in that the antigens are recombinant antigens.

7. A composition according to anyone of claims 1 to 6, characterized in that the antigens and/or fragments thereof are included in fusion proteins.

8. A composition according to anyone of claims 1 to 5, which is substantially free of UreA.

9. A composition according to anyone of claims 1 to 6, which is substantially free of other H. pylori or H. felis antigens.

10. A composition according to anyone of claims 1 to 9, which further contains an adjuvant.

11. A composition according to anyone of claims 1 to 10, which contains a mucosal adjuvant, for example, cholera or E. coli holotoxins.

12. Pharmaceutical composition, characterized in that it comprises, as active ingredient, a composition according to anyone of claims 1 to 10, in combination with physiologically acceptable excipient(s).

13. Composition according to anyone of claims 1 to 11 or pharmaceutical composition according to claim 12, for use as vaccine in protecting an animal or a human host against Helicobacter infection.

14. Composition according to anyone of claims 1 to 11 or pharmaceutical composition according to claim 12, for use as therapeutic or curative treatment of an animal or human host against Helicobacter infection.

15. Composition according to anyone of claims 1 to 11 or pharmaceutical composition according to claim 12, for inducing or enhancing a protective response against mucosal infection by Helicobacter pylori in a host to whom it is administered.

16. Use of H. pylori Hsp antigens for example HspA or HspB, or polypeptides having at least 75 % and preferably 80 to 90 % similarity with said UreB or HspA, or fragments thereof for eliciting a protective response